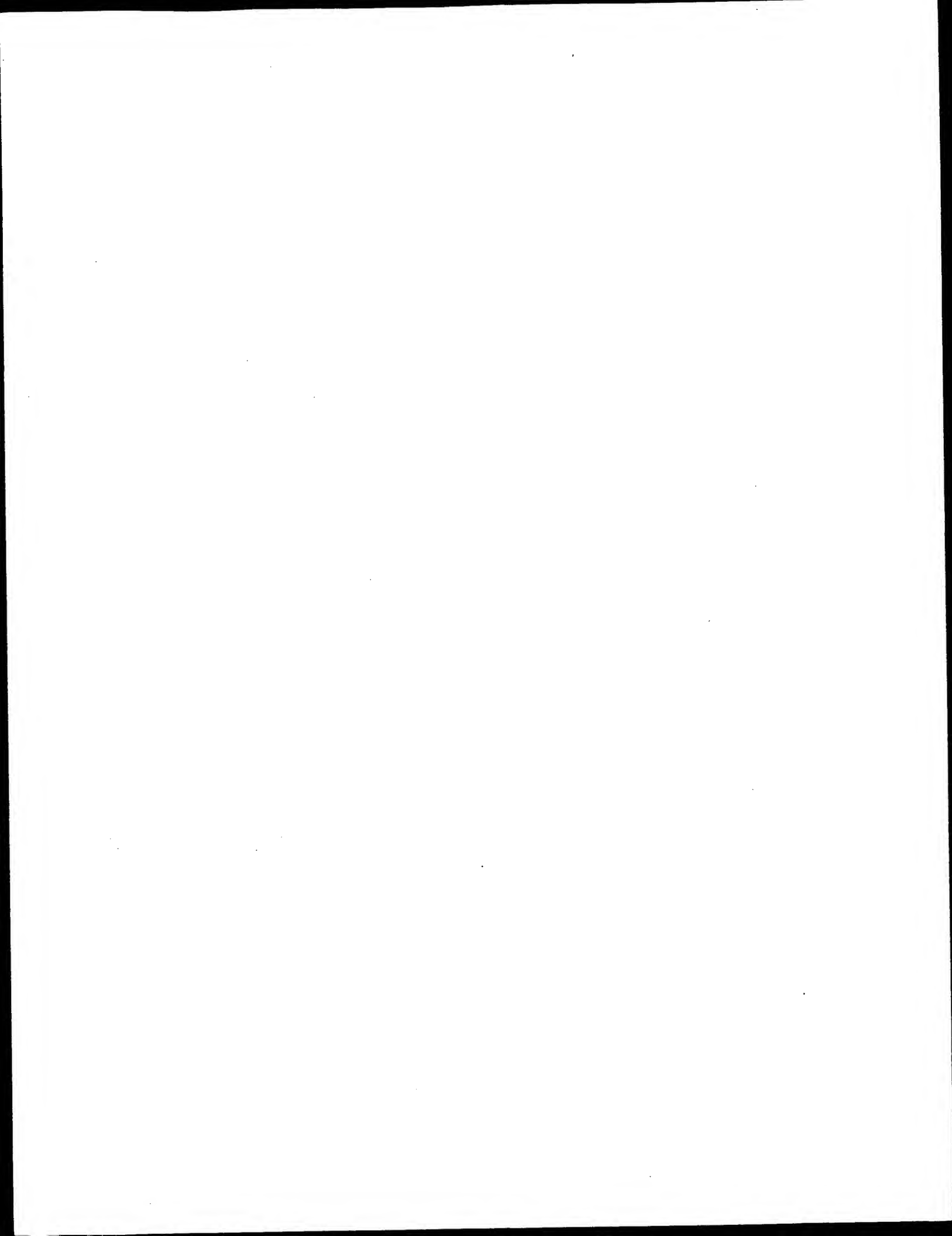


According to the Pre Publication Rules, every patent application received by the United States Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months from the effective filing date. When the application is published the contents, including the sequences, will become prior art.

Two new databases have been created to hold the pre-published sequences:
Published_Applications_NA contains nucleic acid sequences; the search results will have the extension **.rnpb**.
Published_Applications_AA contains amino acid sequences; the search results will have the extension **.rapb**.

Each pre-published application is given a unique Publication Number. An example of a Publication Number is US20021234567A1. The "US" indicates the application was a U.S. application. The first 4 digits show the calendar year the application was published. The next 7 digits represent when the application was published. This 7-digit number starts at zero at the beginning of each calendar year. Each application published is given the next number in order. The "A" indicates a utility patent application and the "1" shows that this was the first time the application had been published. If the applicants submit changes to the application, they may request that the changed application be published again. In such instances, the "1" at the end of the number would be replaced by a "2".

Sequences in the PGPub database are public information; it is permissible to leave these results in the case.



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 10, 2003, 08:32:32 ; Search time 5.91304 Seconds
(without alignments)
99.519 Million cell updates/sec

Title: us-09-910-009a-211

Perfect score: 121

Sequence: 1 XNCCNGGCKXCRDHARCC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.AA.*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	47.9	1417	4	US-08-900-230-3
2	57	47.1	2211	4	US-09-738-884-1
3	54	44.6	58	1	US-08-279-058B-23
4	54	44.6	58	4	US-08-828-323-23
5	53	43.8	40	4	US-09-003-198A-14
6	53	43.8	67	4	US-09-003-198A-16
7	52.5	43.4	1345	2	US-08-977-767-3
8	52.5	43.4	1400	4	US-08-630-915A-37
9	50	41.3	2088	4	US-09-548-372D-13
10	50	41.3	2088	4	US-09-548-367D-13
11	49.5	40.9	54	2	US-08-691-814B-42
12	48.5	40.1	22	1	US-08-599-556-1
13	48.5	40.1	22	5	PCT-US96-05262-2
14	48.5	40.1	27	1	US-08-599-556-7
15	48.5	40.1	27	5	PCT-US96-05262-12
16	48.5	40.1	359	3	US-08-586-185-4
17	48	39.7	170	2	US-08-460-529B-9
18	47	38.8	45	4	US-08-900-230-46
19	47	38.8	45	4	US-08-900-230-53
20	47	38.8	46	4	US-08-900-230-40
21	47	38.8	1833	3	US-08-479-722B-2
22	47	38.8	1833	5	PCT-US95-02251-18
23	46.5	38.4	593	1	US-07-668-648-4
24	46.5	38.4	593	2	US-08-429-998-4
25	46.5	38.4	593	2	US-08-431-333-4
26	46.5	38.4	593	4	US-08-991-862-17
27	46.5	38.4	593	5	PCT-US91-02321-4

28 46.5 38.4 801 1 US-07-906-349A-6
29 46 38.0 25 1 US-08-092-215-4
30 46 38.0 29 1 US-08-092-215-13
31 46 38.0 109 2 US-08-527-044-2
32 46 38.0 109 3 US-09-013-780-2
33 46 38.0 120 3 US-08-508-761B-22
34 46 38.0 162 2 US-08-937-931-10
35 46 38.0 162 4 US-09-285-502-10
36 46 38.0 162 4 US-09-709-126-10
37 46 38.0 162 4 US-09-871-385A-10
38 46 38.0 200 4 US-09-068-740A-2
39 46 38.0 520 4 US-09-068-740A-3
40 46 38.0 702 4 US-09-068-740A-4
41 46 38.0 723 4 US-09-068-740A-9
42 45.5 37.6 713 3 US-08-872-855-5
43 45.5 37.6 720 3 US-08-872-855-4
44 45.5 37.6 722 4 US-08-981-392-12
45 45 37.2 25 1 US-07-789-913-16

ALIGNMENTS

RESULT 1
US-08-900-230-3
; Sequence 3, Application US/08900230
; Patent No. 6329197
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; TITLE OF INVENTION: DNA ENCODING GALANN GALR3 RECEPTORS AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of The Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,230
; FILING DATE: 23-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 52241-C/JPW/ADM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1417 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-900-230-3

Query Match 47.9%; Score 58; DB 4; Length 1417;
Best Local Similarity 50.0%; Pred. No. 28;

Matches 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3 CCNGGCKXCRDHARCC 20

DB 540 CCTGGCGTGGCGACCC 557

Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 CNGGCSKXCRDHARCC 20
| | | | : | | | |
Db 38 CTGGCTACTCGTGAACC 54

RESULT 4
US-08-828-323-23
; Sequence 23, Application US/08828323A
; Patent No. 6413753
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael
; TITLE OF INVENTION: DNA POLYMERASE III HOLOENZYME
; FILE REFERENCE: 19603/10214
; CURRENT APPLICATION NUMBER: US/08/828,323A
; CURRENT FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 23
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Escherichia coli
US-08-828-323-23

Query Match 44.6%; Score 54; DB 4; Length 58;
Best Local Similarity 47.1%; Pred. No. 5.4;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 CNGGCSKXCRDHARCC 20
| | | | : | | | |
Db 38 CTGGCTACTCGTGAACC 54

RESULT 5
US-09-003-198A-14
; Sequence 14, Application US/09003198A
; Patent No. 6316407
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,198A
; FILING DATE: 07-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT.193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids

RESULT 2
US-09-738-884-1
; Sequence 1, Application US/09738884
; Patent No. 6391606
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000849
; CURRENT APPLICATION NUMBER: US/09/738,884
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2211
; TYPE: PRT
; ORGANISM: Human
US-09-738-884-1

Query Match 47.1%; Score 57; DB 4; Length 2211;
Best Local Similarity 50.0%; Pred. No. 52;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 CNGGCSKXCRDHARCC 20
| | | | : | | | |
Db 47 CCGGCTCCGCAAGATCC 64

RESULT 3
US-08-279-058B-23
; Sequence 23, Application US/08279058B
; Patent No. 5668004
; GENERAL INFORMATION:
; APPLICANT: Michael E. O'Donnell
; TITLE OF INVENTION: DNA POLYMERASE III
; TITLE OF INVENTION: HOLOENZYME
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/279,058B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: CRF D-1056CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-279-058B-23

Query Match 44.6%; Score 54; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 5.4;

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-003-198A-14

Query Match 43.8%; Score 53; DB 4; Length 40;
Best Local Similarity 40.7%; Pred. No. 5.1;
Matches 11; Conservative 0; Mismatches 6; Indels 10; Gaps 1;

Qy 4 CNGGCS-----SKXCRDHARC 20
| | | | | | | | | | | | | | | |
Db 14 CFGGCDPHCKTKEHLLSGRCRDRCC 40

RESULT 6

US-09-003-198A-16
Sequence 16, Application US/09003198A
Patent No. 6316407
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip Maganlal
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Hakimi, Salim
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,198A
FILING DATE: 07-JAN-1998
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 16:
LENGTH: 67 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-003-198A-16

Query Match 43.8%; Score 53; DB 4; Length 67;
Best Local Similarity 40.7%; Pred. No. 7.9;
Matches 11; Conservative 0; Mismatches 6; Indels 10; Gaps 1;

Qy 4 CNGGCS-----SKXCRDHARC 20
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Db 41 CFGGCDPHCKTKEHLLSGRCRDRCC 67

RESULT 7

US-08-977-767-3
Sequence 3, Application US/08977767
Patent No. 5972684
GENERAL INFORMATION:
APPLICANT: Bandman, Olga

APPLICANT: Yue, Henry
APPLICANT: Greenwald, Sara
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: CARBONIC ANHYDRASE VIII
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,767
FILING DATE: Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0423 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1532042
US-08-977-767-3

Query Match 43.4%; Score 52.5; DB 2; Length 1345;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

Qy 3 CCGGCSKXKCRDHARC 20
| | | | | | | | | | | | | | | |
Db 774 CCTGGCCATTC-TCAGCC 790

RESULT 8

US-08-630-915A-37
Sequence 37, Application US/08630915A
Patent No. 6309820
GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-8864/9741
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1400 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-630-915A-37

Query Match 43.48; Score 52.5; DB 4; Length 1400;
Best Local Similarity 50.08; Pred. No. 1.1e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 3; Gaps 1;

QY 3 CCGGCSKXCRDHARCC 20
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Db 190 CCGGCA---CTGTACC 204

RESULT 9
US-09-548-372D-13
; Sequence 13, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: US 60/101,594
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 2088
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-13

Query Match 41.3%; Score 50; DB 4; Length 2088;
Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCGGCSKXCRDHARCC 20
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Db 1617 CCTGGACGATCTCCAGCC 1634

RESULT 11
US-08-691-814B-42
; Sequence 42, Application US/08691814B
; Patent No. 5981218
; GENERAL INFORMATION:
; APPLICANT: Rio, Marie-Christine
; APPLICANT: Basset, Paul
; APPLICANT: Byrne, Jennifer
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
; TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,814B
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,183
; FILING DATE: 09-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1383.0090001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 42:
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SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-691-814B-42

Query Match 40.9%; Score 49.5; DB 2; Length 54;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

Qy 3 CCGGCSKXCRDHACC 20
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Db 25 CCHGCIISPSTA-HGRLC 41

RESULT 12
US-08-599-556-1
Sequence 1, Application US/08599556
Patent No. 5670622

GENERAL INFORMATION:
APPLICANT: Shon, Ki-Joon
APPLICANT: Yoshikami, Doju
APPLICANT: Marsh, Maren
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Conotoxin Peptide PIIIA
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005-3917

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,556
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 24260-107674-03
TELEPHONE: 202-962-4848
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus purpurascens

FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Amino acid 1 is pyroglutamate or glutamine."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Amino acid 8 is 4-transhydroxyproline or proline."

FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 4..16
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 5..21
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 11..22
NAME/KEY: Modified-site
LOCATION: 18
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Amino acid 18 is 4-transhydroxyproline or proline."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 22
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "The carboxy terminus may be amidated."
US-08-599-556-1

Query Match 40.1%; Score 48.5; DB 1; Length 22;
Best Local Similarity 45.0%; Pred. No. 9.8;
Matches 9; Conservative 2; Mismatches 6; Indels 3; Gaps 2;

Qy 3 CCGGCSKXCRDHACC 20
||:||||| 1 1 1 1
Db 4 CCGFKXSCRSRQKXH-RCC 22

RESULT 13
PCT-US96-05262-2
Sequence 2, Application PC/TUS9605262
GENERAL INFORMATION:
APPLICANT: Shon, Ki-Joon
APPLICANT: Grilley, Michelle M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Yoshikami, Doju
APPLICANT: Marsh, Maren
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05262
FILING DATE: 17-APR-1996
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/423,561
FILING DATE: 17-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 24260-107674
TELEPHONE: 202-962-4848
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid

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; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 24260-107674-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-599-556-7

Query Match 40.1% Score 48.5; DB 1; Length 27:
Best Local Similarity 45.0%; Pred. No. 12;
Matches 9; Conservative 2; Mismatches 6; Indels

QY 3 CCN--GGCSSKXCRDHARCC 20
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Db 7 CGGFKSCRSRQCKEH-RCC 25

RESULT 15
PCT-US96-05262-12
; Sequence 12, Application PC/TUS9605262
; GENERAL INFORMATION:
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Grille, Michelle M.
; APPLICANT: Oliveira, Baldomero M.
; APPLICANT: Yoshikami, Doju
; APPLICANT: Marsh, Maren
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05262
; FILING DATE: 17-APR-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/423,561
; FILING DATE: 17-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 24260-107674
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-05262-12

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Query Match 40.1%; Score 48.5; DB 5; Length 27;
Best Local Similarity 45.0%; Pred. No. 12;
Matches 9; Conservative 2; Mismatches 6; Indels 3; Gaps 2;

Qy 3 CCN--GGCSSKXCRDHARCC 20
Db 7 CCGFPKSCRSRQCKPH-RCC 25

Search completed: January 10, 2003, 08:38:18
Job time : 7.91304 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2003, 08:33:07 ; Search time 30,9565 Seconds
(without alignments)
12.534 Million cell updates/sec

Title: US-09-910-009a-211

Perfect score: 121

Sequence: 1 XNCCNGCCKXCRDHARCC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	59	48.8	3907	US-10-029-217A-24	Sequence 24, Appli
2	57	47.1	1497	US-09-060-854B-2	Sequence 2, Appli
3	57	47.1	2211	US-10-096-961-1	Sequence 1, Appli
4	55	45.5	1200	US-09-826-508-3	Sequence 3, Appli
5	53.5	44.2	4679	US-09-804-898-2	Sequence 2, Appli
6	52.5	43.4	1400	US-09-879-957-37	Sequence 37, Appli
7	51	42.1	1743	US-10-052-586-451	Sequence 451, Appl
8	50	41.3	42	US-08-969-137-3	Sequence 3, Appli
9	50	41.3	1300	US-10-052-586-269	Sequence 269, Appl
10	50	41.3	1422	US-09-735-933-1	Sequence 1, Appli
11	49	40.5	1435	US-10-052-586-581	Sequence 581, Appl
12	48	39.7	170	US-09-361-736-9	Sequence 9, Appli
13	47	38.8	26	US-09-749-637A-114	Sequence 114, Appl
14	47	38.8	46	US-09-894-882-19	Sequence 19, Appli
15	47	38.8	46	US-09-894-882-58	Sequence 58, Appli
16	47	38.8	46	US-09-894-882-105	Sequence 105, Appl
17	47	38.8	46	US-09-894-882-407	Sequence 407, Appl
18	47	38.8	46	US-09-894-882-426	Sequence 426, Appl
19	47	38.8	46	US-09-894-882-428	Sequence 428, Appl

20	47	38.8	48	10	US-09-894-882-28	Sequence 28, Appli
21	47	38.8	48	10	US-09-894-882-431	Sequence 431, Appl
22	47	38.8	82	10	US-09-894-882-18	Sequence 18, Appli
23	47	38.8	82	10	US-09-894-882-57	Sequence 57, Appli
24	47	38.8	82	10	US-09-894-882-104	Sequence 104, Appl
25	47	38.8	84	10	US-09-894-882-27	Sequence 27, Appli
26	47	38.8	975	10	US-09-886-055-431	Sequence 431, Appl
27	46.5	38.4	593	9	US-09-824-647-17	Sequence 17, Appli
28	46.5	38.4	593	10	US-09-813-156-17	Sequence 17, Appli
29	46.5	38.4	593	10	US-09-824-807-17	Sequence 17, Appli
30	46.5	38.4	621	10	US-09-825-301-1416	Sequence 1416, Ap
31	46.5	38.4	1894	12	US-10-052-586-97	Sequence 97, Appli
32	46	38.0	40	10	US-09-894-882-87	Sequence 87, Appli
33	46	38.0	40	10	US-09-894-882-93	Sequence 93, Appli
34	46	38.0	141	10	US-09-925-300-1686	Sequence 1686, Ap
35	46	38.0	162	10	US-09-871-388-10	Sequence 10, Appli
36	46	38.0	200	10	US-09-995-593A-2	Sequence 2, Appli
37	46	38.0	252	10	US-09-764-903-50	Sequence 50, Appli
38	46	38.0	520	10	US-09-995-593A-3	Sequence 3, Appli
39	46	38.0	702	10	US-09-995-593A-4	Sequence 4, Appli
40	46	38.0	720	10	US-09-756-071B-20	Sequence 20, Appli
41	46	38.0	723	9	US-10-028-072-346	Sequence 346, App
42	46	38.0	723	10	US-09-828-366-21	Sequence 21, Appli
43	46	38.0	723	10	US-09-995-593A-9	Sequence 9, Appli
44	46	38.0	914	9	US-09-975-143-47	Sequence 47, Appli
45	46	38.0	1137	12	US-10-052-586-518	Sequence 518, App

ALIGNMENTS

RESULT 1
US-10-029-217A-24
; Sequence 24, Application US/10029217A
; Patent No. US20020164735A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC N.
; APPLICANT: WANG, DA-ZHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO A CARDIAC-SPECIFIC
; FILE REFERENCE: UTSD:695US
; CURRENT APPLICATION NUMBER: US/10/029,217A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/257,761
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 3907
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-029-217A-24

Query Match 48.8%; Score 59; DB 9; Length 3907;
Best Local Similarity 44.4%; Pred. No. 20;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 CCGCGCCKXCRDHARCC 20

Db 535 CCGCGCAGAGAGCCTCC 552

RESULT 2

US-09-060-854B-2
; Sequence 2, Application US/09060854B
; Patent No. US20020081703A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David Aaron
; TITLE OF INVENTION: Human Protease and Use of Such Protease for Pharmaceutical
; TITLE OF INVENTION: Applications and for Reducing the Allergenicity of No. US2002
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: GC532
; CURRENT APPLICATION NUMBER: US/09/060,854B

; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1497
; TYPE: PRT
; ORGANISM: B. amyloliquefaciens
US-09-060-854B-2

Query Match 47.1%; Score 57; DB 10; Length 1497;

Best Local Similarity 50.0%; Pred. No. 16;

Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

QY 3 CCGGCSKXCRDHARCC 20
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Db 1017 CCGGCGTATCT--ATCC 1032

RESULT 3

US-10-096-961-1
; Sequence 1, Application US/10096961
; Patent No. US2002015572A1
; GENERAL INFORMATION:

; APPLICANT: GUEGLER, Karl et al.
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF

; FILE REFERENCE: CLO00849DIV

; CURRENT APPLICATION NUMBER: US/10/096,961

; CURRENT FILING DATE: 2002-03-14

; PRIOR APPLICATION NUMBER: 60/232,632

; PRIOR FILING DATE: 2000-09-14

; PRIOR APPLICATION NUMBER: 09/738,884

; PRIOR FILING DATE: 2000-12-18

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2211

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-096-961-1

Query Match 47.1%; Score 57; DB 9; Length 2211;

Best Local Similarity 50.0%; Pred. No. 21;

Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 CCGGCSKXCRDHARCC 20
|||: | ||
Db 47 CCGGCTCCGCAAGATCC 64

RESULT 4

US-09-826-508-3

; Sequence 3, Application US/09826508

; Patent No. US2001002509A1

; GENERAL INFORMATION:

; APPLICANT: Nabil Elshourbagy

; APPLICANT: Lisa Vawter

; TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides

; TITLE OF INVENTION: and polynucleotides

; FILE REFERENCE: GP-70744USB

; CURRENT APPLICATION NUMBER: US/09/826,508

; CURRENT FILING DATE: 2001-04-05

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 1200

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-826-508-3

Query Match 45.5%; Score 55; DB 10; Length 1200;

Best Local Similarity 44.4%; Pred. No. 22;

Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
QY 3 CCGGCSKXCRDHARCC 20
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Db 40 CCGGCGAGGTCCGCGGCC 57

RESULT 5

US-09-804-898-2

; Sequence 2, Application US/09804898

; Patent No. US20020045264A1

; GENERAL INFORMATION:

; APPLICANT: DURING, MATTHEW

; APPLICANT: XIAO, WEIDONG

; TITLE OF INVENTION: PRODUCTION OF CHIMERIC CAPSID VECTORS

; FILE REFERENCE: 102182-14

; CURRENT APPLICATION NUMBER: US/09/804,898

; CURRENT FILING DATE: 2001-03-13

; PRIOR APPLICATION NUMBER: 60/189,110

; PRIOR FILING DATE: 2000-03-14

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 4679

; TYPE: PRT

; ORGANISM: adeno-associated virus 2

US-09-804-898-2

Query Match 44.2%; Score 53.5; DB 10; Length 4679;

Best Local Similarity 44.4%; Pred. No. 96;

Matches 8; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

QY 3 CCGGCSKXCRDHARCC 20
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Db 4621 CCGGCGTTTGC-----CC 4633

RESULT 6

US-09-879-957-37

; Sequence 37, Application US/09879957

; Patent No. US20020034755A1

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: HOFFMAN, No. US20020034755A1h

; APPLICANT: KAY, Brian K.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: MCCONNELL, Stephen J.

; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND

; USING SAME

; NUMBER OF SEQUENCES: 227

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/879,957

; FILING DATE: 13-Jun-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/630,915

; FILING DATE: 03-APR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-879-957-37

Query Match 43.4%; Score 52.5; DB 10; Length 1400;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 9; Conservative 1; Mismatches 5; Indels 3; Gaps 1;

QY 3 CCGGCGSSKXCRDHACC 20
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Db 190 CCGGCGCA---CTGTACC 204

RESULT 7
US-10-052-586-451
Sequence 451, Application US/10052586
Patent No. US20020127584A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063734
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063870
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066120
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066466
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069425
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: 60/069870
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/068017
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
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PRIOR FILING DATE: 1998-04-08
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PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
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PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-04-29
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PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/085573

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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
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; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16

;
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089908

Query Match 42.1%; Score 51; DB 12; Length 1743;
Best Local Similarity 44.4%; Pred. No. 83;
Matches 8; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 3 CCNGCCSSKXCRDHARCC 20
|| ||| : | ||
Db 293 CCTGGCCATGCT--CTCC 308

RESULT 8

US-08-969-137-3
; Sequence 3, Application US/08969137
; Patent No. US20010018207A1
; GENERAL INFORMATION:
; APPLICANT: MAYFORD, MARK
; APPLICANT: KANDEL, ERIC
; TITLE OF INVENTION: DNA REGULATORY ELEMENT FOR THE
; TITLE OF INVENTION: EXPRESSION OF TRANSGENES IN NEURONS OF THE MOUSE FOREBRAIN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER AND DUNHAM
; STREET: 1185 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: UNITED STATES
; ZIP: 10036

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,137
; FILING DATE: 12-NOV-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WHITE, JOHN P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/52776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)2276821
; TELEFAX: (212)3910525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

US-08-969-137-3

Query Match 41.3%; Score 50; DB 8; Length 42;
Best Local Similarity 44.4%; Pred. No. 5,5;
Matches 8; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

QY 3 CCNGCCSSKXCRDHARCC 20
|| ||| : | ||
Db 9 CCAGGCAAGC---GCC 22

RESULT 9

US-10-052-586-269
; Sequence 269, Application US/10052586
; Patent No. US20020127584A1
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063564
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063734
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063870
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066120
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066466
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069425
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: 60/069870
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/068017
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083495
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PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086023
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086486
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087098
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087208
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088722
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088740
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088811
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088825
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088863
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089090
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089908

Query Match 41.3%; Score 50; DB 12; Length 1300;
Best Local Similarity 38.9%; Pred. No. 85;
Matches 7; Conservative 1; Mismatches 10; Indels 0; Caps 0;

OY 3 CCGGCSKXCRDHARC 20
||| | | | | | | |
DB 525 CCTGGACATGCTGTACCC 542

RESULT 10
US-09-735-933-1
Sequence 1, Application US/09735933
Patent No. US20020052034A1
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
THEREOF
FILE REFERENCE: CL000863
CURRENT APPLICATION NUMBER: US/09/735,933
CURRENT FILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1422
TYPE: PRT
ORGANISM: Human
US-09-735-933-1

Query Match 41.3%; Score 50; DB 10; Length 1422;

Best Local Similarity 41.2%; Pred. No. 91;
Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 3 CCGGCSKXCRDHARC 19
||| | | | | | | |
DB 1194 CCAGGCATGACTTACAC 1210

RESULT 11
US-10-052-586-581
Sequence 581, Application US/10052586
Patent No. US20020127584A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063564
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063734
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063870
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066120
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066466
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069335

[illegible]

Query Match 40.5%; Score 49; DB 12; Length 1435;
Best Local Similarity 38.9%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCNGCCSKXCRDHARC 20
DB 232 CCTGGAAGAACCATGTC 249

RESULT 12

US-09-361-736-9
; Sequence 9, Application US/09361736
; Patent No. US20020102634A1
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stanniocalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESS: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/361,736
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/460,529
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-361-736-9

Query Match 39.7%; Score 48; DB 10; Length 170;
Best Local Similarity 42.9%; Pred. No. 28;
Matches 9; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

QY 3 CCNG-----GCSKXCRDHARC 19
DB 18 CLNGALQVCCSAFACLDNSTC 38

RESULT 13

US-09-749-637A-114
; Sequence 114, Application US/09749637A
; Patent No. US20020173449A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cartier, G. Edward
; APPLICANT: Watkins, Maren

; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Layer, Richard T.
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
; FILE REFERENCE: 2314-227
; CURRENT APPLICATION NUMBER: US/09/749,637A
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/243,412
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US60/219,440
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/214,263
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/173,754
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 409
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 114
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Conus textile
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(26)
; OTHER INFORMATION: Xaa at residues 3 and 13 may be Pro or hydroxy-Pro; Xaa at res
; OTHER INFORMATION: e 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulp
; OTHER INFORMATION: Tyr or O-phospho-Tyr
US-09-749-637A-114

Query Match 38.8%; Score 47; DB 9; Length 26;
Best Local Similarity 58.3%; Pred. No. 8.2;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 NCCNGGCSKXC 13
DB 14 NCCNGXCVDFIC 25

RESULT 14

US-09-894-882-19
; Sequence 19, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Eisle C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 46
; TYPE: PRT

Fri Jan 10 09:33:20 2003

ORGANISM: Conus radiatus
FEATURE: PEPTIDE
NAME/KEY: (1)..(46)
LOCATION: (1)..(46)
OTHER INFORMATION: Xaa at residues 4, 23, 29, 36 and 42 is Pro or hydroxy-Pro; Xaa at residue 33 is Trp or bromo-Tr
US-09-894-882-19

Query Match 38.8%; Score 47; DB 10; Length 46;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 GCSSKXCRDHARCC 20
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Db 6 GKDGRCRNEADCC 19

RESULT 15
US-09-894-882-58
Sequence 58, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 58
LENGTH: 46
TYPE: PRT
ORGANISM: Conus radiatus
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(46)
OTHER INFORMATION: Xaa at residues 4, 23, 29 and 36 is Pro or hydroxy-Pro
US-09-894-882-58

Query Match 38.8%; Score 47; DB 10; Length 46;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 GCSSKXCRDHARCC 20
| : ||: ||
Db 6 GKDGRCRNEADCC 19

Search completed: January 10, 2003, 08:41:23
Job time : 31.9565 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 10, 2003, 08:32:27 ; Search time 26.2609 Seconds
(without alignments)
101.482 Million cell updates/sec

Title: US-09-910-009A-432

Perfect score: 134

Sequence: 1 ZNCCNGGCGSKWCRDHARC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	133	99.3	75	23	ABB88283
3	117	87.3	20	23	ABB88284
4	111	82.8	22	23	ABB88490
5	110	82.1	76	23	ABB88344
6	94	70.1	22	23	ABB88345
7	85	63.4	22	23	ABB88491
8	85	63.4	74	23	ABB88394
9	84	62.7	26	23	ABB88512
10	84	62.7	80	23	ABB88167

11	83.5	62.3	23	23	ABB88510	C bullatus mu-cono
12	83.5	62.3	77	23	ABB88163	C bullatus mu-cono
13	82	61.2	24	23	ABB88511	C bullatus mu-cono
14	82	61.2	78	23	ABB88165	C bullatus mu-cono
15	75.5	56.3	23	23	ABB88509	C bullatus mu-cono
16	75.5	56.3	77	23	ABB88161	C bullatus mu-cono
17	72	53.7	22	23	ABB88395	C bullatus mu-cono
18	71	52.0	26	23	ABB88168	C bullatus mu-cono
19	70.5	52.6	23	23	ABB88164	C bullatus mu-cono
20	65	48.5	24	23	ABB88166	C bullatus mu-cono
21	63.5	47.4	23	23	ABB88162	C bullatus mu-cono
22	57	42.5	67	22	AAU65054	Propionibacterium
23	57	42.5	155	22	AAU63137	Propionibacterium
24	56.5	42.2	21	23	ABB88300	C tulipa mu-conope
25	56	41.8	397	21	AAG18219	Arabidopsis thalia
26	56	41.8	397	21	AAG54178	Arabidopsis thalia
27	56	41.8	404	23	ABB91272	Herbicidally activ
28	56	41.8	428	23	ABB92485	Herbicidally activ
29	56	41.8	441	21	AAG18218	Arabidopsis thalia
30	56	41.8	441	21	AAG54177	Arabidopsis thalia
31	56	41.8	472	21	AAG18217	Arabidopsis thalia
32	56	41.8	472	21	AAG54176	Arabidopsis thalia
33	55.5	41.4	21	23	ABB88319	C tulipa mu-conope
34	55.5	41.4	21	23	ABB88533	C tulipa mu-conope
35	55.5	41.4	21	23	ABB88534	C tulipa mu-conope
36	55.5	41.4	74	23	ABB88299	C tulipa mu-conope
37	55.5	41.4	75	23	ABB88318	C tulipa mu-conope
38	55	41.0	134	22	ABB44596	Human wound healin
39	55	41.0	175	22	ABB44606	Human wound healin
40	55	41.0	224	22	ABG20306	Novel human diagno
41	54	40.3	57	22	AAU61336	Propionibacterium
42	54	40.3	75	22	AAU39834	Propionibacterium
43	54	40.3	391	21	AAG44312	Arabidopsis thalia
44	54	40.3	391	23	ABB93906	Herbicidally activ
45	54	40.3	404	21	AAG44311	Arabidopsis thalia

ALIGNMENTS

RESULT 1
ABB88449
ID ABB88449 standard; Peptide; 20 AA.
XX
AC ABB88449;
XX
DT 24-MAY-2002 (first entry)
XX
DE C striatus mu-conopeptide SEQ ID NO: 432.
XX
KW Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
KW cerebroprotective; anticonvulsant; antidiabetic;
KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
KW neurodegenerative disease; neuromuscular disorder.
XX
OS Conus striatus.
XX
PN WO200207678-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-US23125.
XX
PR 21-JUL-2000; 2000US-219619P.
PR 03-NOV-2000; 2000US-245157P.
PR 29-JAN-2001; 2001US-264319P.
PR 21-MAR-2001; 2001US-277270P.
XX
PA (UTAH) UNIV UTAH RES FOUND.
PA (COGN-) COGNETIX INC.
XX
PI Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;

PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX WPI; 2002-217020/27.
 XX
 XX New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 XX
 XX Claim 1; Page 85; 231pp; English.
 XX
 XX The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC amyotrophic lateral sclerosis, trigeminal neuralgia, diabetic neuropathy,
 CC severe chronic pain, stroke, neuronal pain and phantom limb, burn pain,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide of the invention.
 XX
 XX Sequence 20 AA;
 SQ
 Query Match 100.0%; Score 134; DB 23; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ZNCCNGGCGSSKWCGRDHARCC 20
 DB 1 ZNCCNGGCGSSKWCGRDHARCC 20
 RESULT 2
 ABB88283
 ID ABB88283 standard; Protein; 75 AA.
 XX
 XX ABB88283;
 XX
 XX 24-MAY-2002 (first entry)
 DT
 DE C striatus mu-conopeptide S3-2 propeptide.
 XX
 XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.
 XX
 XX Conus striatus.
 OS
 XX
 XX WO200207678-A2.
 XX
 XX 31-JAN-2002.
 XX
 XX 23-JUL-2001; 2001WO-US23125.
 XX
 XX 21-JUL-2000; 2000US-219619P.
 PR 03-NOV-2000; 2000US-245157P.
 PR 29-JAN-2001; 2001US-264319P.
 PR 21-MAR-2001; 2001US-277270P.
 XX
 XX (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX
 XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX
 XX WPI; 2002-217020/27.
 XX
 XX N-PSDB; ABL88549.
 DR

XX
 PT New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 XX
 XX Claim 9; Page 56; 231pp; English.
 XX
 XX The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC amyotrophic lateral sclerosis, trigeminal neuralgia, diabetic neuropathy,
 CC severe chronic pain, stroke, neuronal pain and phantom limb, burn pain,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide preprotein of the invention.
 XX
 XX Sequence 75 AA;
 SQ
 Query Match 99.3%; Score 133; DB 23; Length 75;
 Best Local Similarity 95.0%; Pred. No. 1.2e-07;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ZNCCNGGCGSSKWCGRDHARCC 20
 DB 54 QNCCNGGCGSSKWCGRDHARCC 73
 RESULT 3
 ABB88284
 ID ABB88284 standard; Peptide; 20 AA.
 XX
 XX ABB88284;
 XX
 XX 24-MAY-2002 (first entry)
 DT
 DE C striatus mu-conopeptide S3-2.
 XX
 XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.
 XX
 XX Conus striatus.
 OS
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1 /label= Gln, OTHER
 FT /note= "OTHER=pyroglu"
 FT Misc-difference 12 /label= Trp, OTHER
 FT /note= "bromo-Trp"
 XX
 XX WO200207678-A2.
 XX
 XX 31-JAN-2002.
 XX
 XX 23-JUL-2001; 2001WO-US23125.
 XX
 XX 21-JUL-2000; 2000US-219619P.
 PR 03-NOV-2000; 2000US-245157P.
 PR 29-JAN-2001; 2001US-264319P.
 PR 21-MAR-2001; 2001US-277270P.
 XX
 XX (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX

PI Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 DR WPI: 2002-217020/27.
 XX
 PT New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 XX
 PS Claim 1; Page 56; 231pp; English.

XX The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC anytrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide of the invention.
 XX
 SQ Sequence 20 AA;

Query Match 87.3%; Score 117; DB 23; Length 20;
 Best Local Similarity 94.7%; Pred. No. 2.2e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 NCCNGCCKWCRDHARCC 20
 DB 2 NCCNGCCKWCRDHARCC 20
 ||||| ||||| |||||

RESULT 4
 ABB88490
 ID ABB88490 standard; Peptide: 22 AA.

XX ABB88490;
 XX
 DT 24-MAY-2002 (first entry)
 XX
 DE C stercusmuscarum mu-conopeptide SEQ ID NO: 473.
 XX
 KW Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.
 XX

OS Conus stercusmuscarum.
 XX
 PN WO200207678-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 23-JUL-2001; 2001WO-US23125.
 XX
 PR 21-JUL-2000; 2000US-219619P.
 PR 03-NOV-2000; 2000US-245157P.
 PR 29-JAN-2001; 2001US-264319P.
 PR 21-MAR-2001; 2001US-277270P.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.

XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX
 DR WPI: 2002-217020/27.

XX New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 XX
 PS Claim 1; Page 83; 231pp; English.

XX The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC anytrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide of the invention.
 XX
 SQ Sequence 22 AA;

Query Match 82.8%; Score 111; DB 23; Length 22;
 Best Local Similarity 77.3%; Pred. No. 1e-05;
 Matches 17; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 ZNCCNG--GCSSKWCARDHARCC 20
 DB 1 ZRCCNGRCSSKWCARDHARCC 22
 ||||| ||||| ||||| |||||

RESULT 5
 ABB88344
 ID ABB88344 standard; Protein: 76 AA.

XX ABB88344;
 XX
 DT 24-MAY-2002 (first entry)
 XX
 DE C stercusmuscarum mu-conopeptide Sm3-3 propeptide.
 XX
 KW Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.
 XX
 OS Conus stercusmuscarum.
 XX
 PN WO200207678-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 23-JUL-2001; 2001WO-US23125.
 XX
 PR 21-JUL-2000; 2000US-219619P.
 PR 03-NOV-2000; 2000US-245157P.
 PR 29-JAN-2001; 2001US-264319P.
 PR 21-MAR-2001; 2001US-277270P.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.

XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX
 DR WPI: 2002-217020/27.
 DR N-PSDB: ABL88578.
 XX
 PT New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular

PT blocking agents, as local anesthetic agents, as analgesic agents and as
PT neuroprotective agents -
XX Claim 9; Page 69; 231pp; English.
XX The present invention relates to mu-conopeptides derived from snails,
CC which can be in the treatment of disorders associated with voltage-gated
CC ion channels. These may include neurodegenerative disorders such as
CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
CC or ischaemia which typically follows stroke, cerebrovascular accident,
CC brain or spinal cord trauma, myocardial infarct, physical trauma,
CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
CC providing muscle relaxation, treating essential blepharospasm and other
CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
CC is a mu-conopeptide preprotein of the invention.
XX
XX Sequence 76 AA;
XX
XX Query Match 82.1%; Score 110; DB 23; Length 76;
XX Best Local Similarity 72.7%; Pred. No. 3.6e-05;
XX Matches 16; Conservative 3; Mismatches 1; Indels 2; Gaps 1;
XX
XX QY 1 ZNCCNG--GCSSKWCGRDHARCC 20
XX : |||| |||||:||||:||||
XX Db 52 ORCCNGRCSSRXCGRDHARCC 73
XX
XX RESULT 6
XX ABB88345
XX ID ABB88345 standard; Peptide; 22 AA.
XX AC ABB88345;
XX DT 24-MAY-2002 (first entry)
XX
XX C stercusmuscarum mu-conopeptide Sm3-3.
XX
XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
XX anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
XX cerebroprotective; anticonvulsant; antitachycardic; antidiabetic;
XX cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
XX neurodegenerative disease; neuromuscular disorder.
XX
XX Conus stercusmuscarum.
XX
XX Key Location/Qualifiers
XX Misc-difference 1 /label= Gln, OTHER
XX FT /note= "OTHER=pyroglu"
XX FT Misc-difference 14 /label= Trp, OTHER
XX FT /note= "OTHER=bromo-Trp"
XX
XX WO200207678-A2.
XX
XX 31-JAN-2002.
XX
XX 23-JUL-2001; 2001WO-US23125.
XX
XX 21-JUL-2000; 2000US-219619P.
XX 03-NOV-2000; 2000US-245157P.
XX 29-JAN-2001; 2001US-264319P.
XX 21-MAR-2001; 2001US-277270P.
XX
XX (UTAH) UNIV UTAH RES FOUND.
XX (COGN-) COGNETIX INC.
XX
XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
XX Jacobsen R, Jones RM, Cartier GE, Shen GS;
XX
XX WPI; 2002-217020/27.

DR WPI; 2002-217020/27.
XX New mu-conopeptides useful for treating disorders associated with
PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
PT blocking agents, as local anesthetic agents, as analgesic agents and as
PT neuroprotective agents -
XX Claim 1; Page 69; 231pp; English.
XX The present invention relates to mu-conopeptides derived from snails,
CC which can be in the treatment of disorders associated with voltage-gated
CC ion channels. These may include neurodegenerative disorders such as
CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
CC or ischaemia which typically follows stroke, cerebrovascular accident,
CC brain or spinal cord trauma, myocardial infarct, physical trauma,
CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
CC providing muscle relaxation, treating essential blepharospasm and other
CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
CC is a mu-conopeptide of the invention.
XX
XX Sequence 22 AA;
XX
XX Query Match 70.1%; Score 94; DB 23; Length 22;
XX Best Local Similarity 75.0%; Pred. No. 0.00071;
XX Matches 15; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
XX
XX QY 3 CCNG--GCSSKWCGRDHARCC 20
XX : |||| |||||:||||:||||
XX Db 3 CCNGRCSSRXCGRDHARCC 22
XX
XX RESULT 7
XX ABB88491
XX ID ABB88491 standard; Peptide; 22 AA.
XX AC ABB88491;
XX DT 24-MAY-2002 (first entry)
XX
XX C consors mu-conopeptide SEQ ID NO: 474.
XX
XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
XX anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
XX cerebroprotective; anticonvulsant; antitachycardic; antidiabetic;
XX cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
XX neurodegenerative disease; neuromuscular disorder.
XX
XX Conus consors.
XX
XX WO200207678-A2.
XX
XX 31-JAN-2002.
XX
XX 23-JUL-2001; 2001WO-US23125.
XX
XX 21-JUL-2000; 2000US-219619P.
XX 03-NOV-2000; 2000US-245157P.
XX 29-JAN-2001; 2001US-264319P.
XX 21-MAR-2001; 2001US-277270P.
XX
XX (UTAH) UNIV UTAH RES FOUND.
XX (COGN-) COGNETIX INC.
XX
XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
XX Jacobsen R, Jones RM, Cartier GE, Shen GS;
XX
XX WPI; 2002-217020/27.

New mu-conopeptides useful for treating disorders associated with
voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular

PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 PS
 PS Claim 1; Page 83; 231pp; English.
 XX
 CC The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide of the invention.

SQ Sequence 22 AA;
 Query Match 63.4%; Score 85; DB 23; Length 22;
 Best Local Similarity 60.0%; Pred. No. 0.0067;
 Matches 12; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 3 CCN--GGCSKWCGRDHARCC 20
 II: ||: |||||: ||
 Db 3 CCDVPNACSGRWCRDHAQCC 22

RESULT 8
 ABB88394
 ID ABB88394 standard; Protein; 74 AA.
 AC
 AC ABB88394;

24-MAY-2002 (first entry)
 C consors mu-conopeptide Cn3-3 propeptide.

Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 neurodegenerative disease; neuromuscular disorder.

Conus consors.
 OS
 WO200207678-A2.
 PN
 XX
 XX 31-JAN-2002.
 XX
 XX 23-JUL-2001; 2001WO-US23125.
 XX
 XX 21-JUL-2000; 2000US-219619P.
 XX
 XX 03-NOV-2000; 2000US-245157P.
 XX
 XX 29-JAN-2001; 2001US-264319P.
 XX
 XX 21-MAR-2001; 2001US-277270P.
 XX
 XX (UTAH) UNIV UTAH RES FOUND.
 XX
 XX (COGN-) COGNETIX INC.

XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 XX Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX
 XX WPI; 2002-217020/27.
 XX N-PSDB; ABL88603.

XX New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 XX

PS Claim 9; Page 80; 231pp; English.
 XX
 CC The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide preprotein of the invention.

SQ Sequence 74 AA;
 Query Match 63.4%; Score 85; DB 23; Length 74;
 Best Local Similarity 60.0%; Pred. No. 0.018;
 Matches 12; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 3 CCN--GGCSKWCGRDHARCC 20
 II: ||: |||||: ||
 Db 54 CCDVPNACSGRWCRDHAQCC 73

RESULT 9
 ABB88512
 ID ABB88512 standard; Peptide; 26 AA.
 AC
 AC ABB88512;

24-MAY-2002 (first entry)

C bullatus mu-conopeptide SEQ ID NO: 495.

Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 neurodegenerative disease; neuromuscular disorder.

Conus bullatus.
 OS
 WO200207678-A2.
 PN
 XX
 XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US23125.
 XX
 XX 21-JUL-2000; 2000US-219619P.
 XX
 XX 03-NOV-2000; 2000US-245157P.
 XX
 XX 29-JAN-2001; 2001US-264319P.
 XX
 XX 21-MAR-2001; 2001US-277270P.
 XX
 XX (UTAH) UNIV UTAH RES FOUND.
 XX
 XX (COGN-) COGNETIX INC.

XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 XX Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX
 XX WPI; 2002-217020/27.

XX New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 XX

Claim 1; Page 84; 231pp; English.

The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated

CC ion channels. These may include neurodegenerative disorders such as
 CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide of the invention.

XX SQ Sequence 26 AA;

Query Match 62.7%; Score 84; DB 23; Length 26;

Best Local Similarity 56.0%; Pred. No. 0.0099;

Matches 14; Conservative 3; Mismatches 2; Indels 6; Gaps 2;

QY 1 ZNCCN-----GGCSSKWCGRDHARCC 20

: ||| || : |||||: |||

Db 3 DRCCNKGNGKRGK-SRWCRDHSRCC 26

RESULT 10

ABB88167

ID ABB88167 standard; Protein; 80 AA.

XX AC

XX ABB88167;

DT 24-MAY-2002 (first entry)

DE C bullatus mu-conopeptide Bu3-3 propeptide.

XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.

XX OS Conus bullatus.

XX WO200207678-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US23125.

XX 21-JUL-2000; 2000US-219619P.

XX 03-NOV-2000; 2000US-245157P.

XX 29-JAN-2001; 2001US-264319P.

XX 21-MAR-2001; 2001US-277270P.

XX (UTAH) UNIV UTAH RES FOUND.

XX (COGN-) COGNETIX INC.

XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;

XX Jacobsen R, Jones RM, Cartier GE, Shen GS;

XX WPI; 2002-217020/27.

XX N-PSDB; ABL88496.

XX New mu-conopeptides useful for treating disorders associated with

XX voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular

XX blocking agents, as local anesthetic agents, as analgesic agents and as

XX neuroprotective agents -

XX Claim 9; Page 29; 231pp; English.

XX The present invention relates to mu-conopeptides derived from snails,

XX which can be in the treatment of disorders associated with voltage-gated

XX ion channels. These may include neurodegenerative disorders such as

XX amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or

XX severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,

CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide preprotein of the invention.

XX SQ Sequence 80 AA;

Query Match 62.7%; Score 84; DB 23; Length 80;

Best Local Similarity 56.0%; Pred. No. 0.024;

Matches 14; Conservative 3; Mismatches 2; Indels 6; Gaps 2;

QY 1 ZNCCN-----GGCSSKWCGRDHARCC 20

: ||| || : |||||: |||

Db 54 DRCCNKGNGKRGK-SRWCRDHSRCC 77

RESULT 11

ABB88510

ID ABB88510 standard; Peptide; 23 AA.

XX AC

XX ABB88510;

XX 24-MAY-2002 (first entry)

XX C bullatus mu-conopeptide SEQ ID NO: 493.

XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;

XX anaesthetic; neuromuscular blocking agent; neuroprotective; pain;

XX cerebroprotective; anticonvulsant; antidiabetic;

XX cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;

XX neurodegenerative disease; neuromuscular disorder.

XX OS Conus bullatus.

XX WO200207678-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US23125.

XX 21-JUL-2000; 2000US-219619P.

XX 03-NOV-2000; 2000US-245157P.

XX 29-JAN-2001; 2001US-264319P.

XX 21-MAR-2001; 2001US-277270P.

XX (UTAH) UNIV UTAH RES FOUND.

XX (COGN-) COGNETIX INC.

XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;

XX Jacobsen R, Jones RM, Cartier GE, Shen GS;

XX WPI; 2002-217020/27.

XX New mu-conopeptides useful for treating disorders associated with

XX voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular

XX blocking agents, as local anesthetic agents, as analgesic agents and as

XX neuroprotective agents -

XX Claim 1; Page 84; 231pp; English.

XX The present invention relates to mu-conopeptides derived from snails,

XX which can be in the treatment of disorders associated with voltage-gated

XX ion channels. These may include neurodegenerative disorders such as

XX amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or

XX severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,

XX post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,

XX epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia

XX or ischaemia which typically follows stroke, cerebrovascular accident,

XX brain or spinal cord trauma, myocardial infarct, physical trauma,

CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide of the invention.

XX Sequence 23 AA;
 SQ Query Match 62.3%; Score 83.5; DB 23; Length 23;
 Best Local Similarity 59.1%; Pred. No. 0.01;
 Matches 13; Conservative 3; Mismatches 3; Indels 3; Gaps 2;

QY 1 ZNCCNG--GCSSKWCGRDHARCC 20
 Db 3 DRCKGKRGCG--GRWCRDHSRCC 23

RESULT 12
 ABB88163
 ID ABB88163 standard; Protein; 77 AA.

XX ABB88163;

DT 24-MAY-2002 (first entry)

DE C bullatus mu-conopeptide Bu3-1A propeptide.

XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiac; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.

XX Conus bullatus.

OS WO200207678-A2.

PN 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US23125.

XX 21-JUL-2000; 2000US-219619P.

XX 03-NOV-2000; 2000US-245157P.

XX 29-JAN-2001; 2001US-264319P.

XX 21-MAR-2001; 2001US-277270P.

XX (UTAH) UNIV UTAH RES FOUND.

PA (COGN-) COGNETIX INC.

XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE, Shen GS;

DR WPI; 2002-217020/27.

XX N-PSDB; ABL88494.

XX New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents

PS Claim 9; Page 28; 231pp; English.

XX The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence

CC is a mu-conopeptide preprotein of the invention.
 XX Sequence 77 AA;
 SQ Query Match 62.3%; Score 83.5; DB 23; Length 77;
 Best Local Similarity 59.1%; Pred. No. 0.027;
 Matches 13; Conservative 3; Mismatches 3; Indels 3; Gaps 2;

QY 1 ZNCCNG--GCSSKWCGRDHARCC 20
 Db 54 DRCKGKRGCG--GRWCRDHSRCC 74

RESULT 13
 ABB88511
 ID ABB88511 standard; Peptide; 24 AA.

XX ABB88511;

DT 24-MAY-2002 (first entry)

DE C bullatus mu-conopeptide SEQ ID NO: 494.

XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiac; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.

XX Conus bullatus.

OS WO200207678-A2.

PN 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US23125.

XX 21-JUL-2000; 2000US-219619P.

XX 03-NOV-2000; 2000US-245157P.

XX 29-JAN-2001; 2001US-264319P.

XX 21-MAR-2001; 2001US-277270P.

XX (UTAH) UNIV UTAH RES FOUND.

PA (COGN-) COGNETIX INC.

XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE, Shen GS;

DR WPI; 2002-217020/27.

XX New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents

PS Claim 1; Page 84; 231pp; English.

XX The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide of the invention.

XX Sequence 24 AA;

us-09-910-009a-432.rag

Fri Jan 10 09:33:21 2003

Search completed: January 10, 2003, 08:35:36
Job time : 27.5942 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 10, 2003, 08:32:32 ; Search time 6.43478 Seconds
(without alignments)
298.796 Million cell updates/sec

Title: US-09-910-009a-432

Perfect score: 134

Sequence: 1 ZNCCNGCGSKWCRDHARCC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	40.3	362	2 T52038	probable phytochel
2	53.5	39.9	258	2 F72616	hypothetical prote
3	53	39.6	223	2 B38346	ultra-high-sulfur
4	53	39.6	230	2 A38346	ultra-high-sulfur
5	52	38.8	169	1 S18946	ultra-high-sulfur
6	51.5	38.4	63	2 A34484	metallothionein I
7	51.5	38.4	2910	2 T42214	otogelin - mouse
8	51	38.1	454	2 H86231	hypothetical prote
9	50.5	37.7	591	2 I48141	acroganin - guine
10	50	37.3	389	2 T46722	conserved hypothe
11	50	37.3	471	1 KHRZOB	oryzain (EC 3.4.22
12	50	37.3	1115	2 S40241	G protein-coupled
13	48.5	36.2	71	2 S47576	metallothionein 20
14	48.5	36.2	71	2 S39420	metallothionein 20
15	48.5	36.2	71	2 S39421	metallothionein 20
16	48.5	36.2	147	2 T49670	hypothetical prote
17	48.5	36.2	152	2 T18975	hypothetical prote
18	48.5	36.2	164	2 T24272	hypothetical prote
19	48.5	36.2	404	2 E96745	hypothetical prote
20	48.5	36.2	493	2 T01206	cysteine proteinas
21	48	35.8	73	2 G87164	hypothetical prote
22	48	35.8	477	1 DWDXAF	2-hydroxyglutaryl-
23	48	35.8	695	2 A38314	L-amino-acid oxida
24	48	35.8	719	2 T00266	hypothetical prote
25	47.5	35.4	188	2 JC6547	high sulfur protei
26	47.5	35.4	302	2 T00480	probable RING zinc
27	47.5	35.4	1172	2 F84572	probable cadmium-t
28	47	35.1	115	2 A36113	antileukoproteinas
29	47	35.1	172	2 F96566	F6D8.19 [imported]

hypothetical prote
hypothetical prote
probable phytochel
cysteine proteinas
hypothetical prote
neuronal apoptosis
granulin precursor
metallothionein I
hypothetical prote
Beta-microseminopr
epididymis-specifi
hypothetical prote
cysteine proteinas
late competence pr
cysteine proteinas
transponson protei

ALIGNMENTS

RESULT 1

T52038

probable phytochelatin synthetase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000

C:Accession: T52038

R:Zimmermann, M.

submitted to the EMBL Data Library, June 1998

A:Reference number: Z25914

A:Accession: T52038

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-362 <ZIM>

A:Cross-references: EMBL:AJ006787; PIDN:CAA07251.1

A:Experimental source: seedlings

Query Match 40.3%; Score 54; DB 2; Length 362;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 NCCNGCGSKWCRDHA 17

Db 44 NCKGGVMNSWQDPA 59

RESULT 2

F72616

hypothetical protein APE1391 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C:Accession: F72616

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Jin-no, K.;

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, Y.; Yamazaki, J.

DNA Res. 6, 83-101, 1999

A>Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: F72616

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-258 <KAW>

A:Cross-references: DBJ:AP000061; NID:g5104821; PIDN:BAA80388.1; PID:g5105074

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE1391

C:Superfamily: Aeropyrum pernix hypothetical protein APE1391

Query Match 39.9%; Score 53.5; DB 2; Length 258;
Best Local Similarity 47.1%; Pred. No. 20;
Matches 8; Conservative 1; Mismatches 3; Indels 5; Gaps 1;

QY 4 CNGCGSKWCRDHARCC 20

Db 44 NCKGGVMNSWQDPA 59


```

A:Cross-References: GB:M86735; NID:g191234; PIDN:AAA37030.1; PID:g191233
C:Superfamily: granulin

Query Match          37.7%; Score 50.5; DB 2; Length 591;
Best Local Similarity 33.3%; Pred. No. 77;
Matches 10; Conservative 1; Mismatches 8; Indels 11; Gaps 2;

QY 1 ZNCNGGCSKSW-----CRDHARCC 20
      :|||      |||
      :|||      |||
Db 293 QTCRQLQ-SGKWCCPFPKAVCCEDHVHCC 321

RESULT 10
T46722
conserved hypothetical protein [imported] - Leishmania major
N:Alternate names: probable proline synthetase associated protein
C:Species: Leishmania major
C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C:Accession: T46722
R:Volckaert, G.; Ivens, A.C.; Lawson, D.; Quail, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, December 1999
A:Reference number: Z2137
A:Accession: T46722
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-389 <VOL>
A:Cross-References: EMBL:AL121861; PIDN:CAB58387.1
A:Experimental source: strain Friedlin
C:Genetics:
A:Note: L4326.11

Query Match          37.3%; Score 50; DB 2; Length 389;
Best Local Similarity 44.4%; Pred. No. 67;
Matches 8; Conservative 1; Mismatches 5; Indels 4; Gaps 1;

QY 3 CCNGGCSKWCRRHARCC 20
      ||| |||      | |||
      ||| |||      | |||
Db 78 CCSAGC----CLCHVDCC 91

RESULT 11
KHZ0B
oryzaain (EC 3.4.22.-) beta precursor - rice
C:Species: Oryza sativa (rice)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jun-2000
C:Accession: J00389; B40053
C:Watanabe, H.; Abe, K.; Emori, Y.; Hosoyama, H.; Arai, S.

```

A:Molecule type: mRNA
A:Residues: 1-471 <WAT1>
R:Watanabe, H.; Abe, K.; Emori, Y.: Hosoyama, H.; Arai, S.
J. Biol. Chem. 266, 16897-16902, 1991
A:Title: Molecular cloning and gibberellin-induced expression of multiple cysteine proteinase genes from *Pinus densata*
A:Reference number: A40053; MUID: 91358494; PMID:1885617
A:Accession: B40053
A:Molecule type: mRNA
A:Residues: 1-471 <WAT2>
A:Cross-references: GB:D90407; NID:g218182; PIDN:BAAL14403.1; PID:g218183
C:Superfamily: papain
C:Keywords: cysteine proteinase; glycoprotein; hydrolase; seed
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-139/Domain: amino-terminal propeptide #status predicted <PRO>
F:140-360/Product: oryzanin beta #status predicted <MAT>
F:361-471/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:161-204,195-237,295-346/Disulfide bonds: #status predicted
F:164,301,321/Active site: Cys, His, Asn #status predicted
F:340,388/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	37.3%	Score 50;	DB 1;	Length 471;
Best Local Similarity	40.9%	Pred. No. 76;		
Matches	9;	Conservative	2;	Mismatches 7;
				Indels 4;
				Gaps 1;

QY 3 CCNGGC-----SSKWCGRDHACC 20
| | | | | : | | | | |
Db 407 CLVWGCPVEGATCCRDHASC 428

RESULT 12

S40241
G protein-coupled receptor - great pond snail
C:Species: Lymnaea stagnalis (great pond snail)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C:Accession: S40241
R:Tensen, C.P.; Kesteren, E.R.; Planta, R.J.; Cox, K.; Burke, J.F.; Heerikhuizen, H.; Vri
submitted to the EMBL Data Library, June 1993
A:Description: A G protein-coupled receptor with LDL-binding motifs suggests a role for
A:Reference number: S40241

A:Accession: S40241
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1115 <TEN>
A:Cross-references: EMBL:Z23104; NID:g438128; PID:g438129
C:Superfamily: great pond snail LDL receptor-related G protein-coupled receptor: LDL rec
C:Keywords: G protein-coupled receptor; transmembrane protein
F:38-77/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:79-113/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:118-153/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:158-194/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:195-230/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F:233-267/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F:274-316/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F:322-361/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F:367-401/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F:406-440/Domain: LDL receptor ligand-binding repeat homology <LDL10>
F:446-483/Domain: LDL receptor ligand-binding repeat homology <LDL11>
F:488-523/Domain: LDL receptor ligand-binding repeat homology <LDL12>
F:584-607/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:608-631/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:632-655/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:656-679/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:704-727/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:774-797/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

Query Match 37.3%; Score 50; DB 2; Length 1115;
Best Local Similarity 38.1%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 1 ZNCNGGC--SSKWCGRDHACC 19
: | | | | | | | | | |
Db 411 KSCLSGHCIEHKWCFHREC 431

RESULT 13

S47576
metallothionein 20-Ib - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 17-Mar-1999
C:Accession: S47576
R:Mackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; R
Eur. J. Biochem. 218, 183-194, 1993
A:Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal
A:Reference number: S39416; MUID:94062828; PMID:8243463
A:Accession: S47576

A:Molecule type: protein
A:Residues: 1-71 <MAC>
C:Superfamily: metallothionein
C:Keywords: chelation; metal binding

Query Match 36.2%; Score 48.5; DB 2; Length 71;
Best Local Similarity 40.7%; Pred. No. 33;
Matches 11; Conservative 1; Mismatches 6; Indels 9; Gaps 2;

QY 2 NC-----CNGGSSKWCGR--DHARC 19
| | | | | | | | | | | |

Db 5 NCETNVICIGTGGCGKCCRCGDACKC 31

RESULT 14

S39420
metallothionein 20-Ia - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C:Accession: S39420
R:Mackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.
Eur. J. Biochem. 218, 183-194, 1993
A:Title: Complete amino acid sequences of five dimeric and four monomeric forms of me
A:Reference number: S39416; MUID:94062828; PMID:8243463
A:Accession: S39420

A:Molecule type: protein
A:Residues: 1-71 <MAC>
C:Superfamily: metallothionein
C:Keywords: chelation; metal binding

Query Match 36.2%; Score 48.5; DB 2; Length 71;
Best Local Similarity 40.7%; Pred. No. 33;
Matches 11; Conservative 1; Mismatches 6; Indels 9; Gaps 2;

QY 2 NC-----CNGGSSKWCGR--DHARC 19
| | | | | | | | | | | |
Db 5 NCETNVICIGTGGCGKCCRCGDACKC 31

RESULT 15

S39421
metallothionein 20-II - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C:Accession: S39421
R:Mackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.
Eur. J. Biochem. 218, 183-194, 1993
A:Title: Complete amino acid sequences of five dimeric and four monomeric forms of me
A:Reference number: S39416; MUID:94062828; PMID:8243463
A:Accession: S39421

A:Molecule type: protein
A:Residues: 1-71 <MAC>
C:Superfamily: metallothionein
C:Keywords: chelation; metal binding

Query Match 36.2%; Score 48.5; DB 2; Length 71;
Best Local Similarity 40.7%; Pred. No. 33;
Matches 11; Conservative 1; Mismatches 6; Indels 9; Gaps 2;

QY 2 NC-----CNGGSSKWCGR--DHARC 19
| | | | | | | | | | | |
Db 5 NCETNVICIGTGGCGKCCRCGDACKC 31

Search completed: January 10, 2003, 08:36:23
Job time : 7.43478 secs

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OM protein - protein search, using sw model

Run on: January 10, 2003, 08:32:27 ; Search time 98.4783 Seconds
(without alignments)
101.482 Million cell updates/sec

Title: US-09-910-009A-210
Perfect score: 420
Sequence: 1 G5MMSKLGVLTVCLLLFPL.....CNGCGCKSKWCRDHRCGR 75

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	420	100.0	75	23	ABB88283
2	372	88.6	76	23	ABB88344
3	335	79.8	74	23	ABB88394
4	320	76.2	80	23	ABB88167
5	306.5	73.0	76	23	ABB88396
6	306	72.9	78	23	ABB88105
7	304.5	72.5	75	23	ABB88318
8	303.5	72.3	78	23	ABB88149
9	303.5	72.3	78	23	ABB88261
10	299.5	71.3	74	23	ABB88299
					C striatus mu-cono
					C stercusmuscarum
					C consors mu-cono
					C bullatus mu-cono
					C consors mu-cono
					C bullatus mu-cono
					C tulipa mu-cono
					C aurisilacus mu-co
					C nobilis mu-conop
					C tulipa mu-conope

11	299.5	71.3	77	23	ABB88163	C bullatus mu-cono
12	293.5	69.9	76	23	ABB88320	C aurisilacus mu-co
13	292.5	69.6	75	23	ABB88277	C stercusmuscarum
14	292.5	69.6	77	23	ABB88161	C bullatus mu-cono
15	277.5	66.1	74	23	ABB88238	C magus mu-conopep
16	271.5	64.6	74	23	ABB88236	C magus mu-conopep
17	271.5	64.6	75	23	ABB88328	C parius mu-conope
18	270.5	64.4	74	23	ABB88189	C parius mu-conope
19	269.5	64.2	77	23	ABB88169	C circuncisus mu-c
20	267.5	63.7	74	23	ABB88177	C bullatus mu-cono
21	267.5	63.7	74	23	ABB88232	C characteristicus
22	267	63.6	75	23	ABB88179	C characteristicus
23	267	63.6	75	23	ABB88205	C geographus mu-co
24	267	63.6	73	23	ABB88230	C magus mu-conopep
25	266.5	63.3	73	23	ABB88279	C stercusmuscarum
26	266	63.3	75	23	ABB88147	C aurisilacus mu-co
27	266	63.3	76	23	ABB88326	C parius mu-conope
28	264	62.9	75	23	ABB88207	C geographus mu-co
29	263	62.6	72	23	ABB88193	C dalli mu-conopep
30	262.5	62.5	75	23	ABB88342	C rattus mu-conope
31	262	62.4	68	23	ABB88244	C marmoreus mu-con
32	260	61.9	76	23	ABB88242	C marmoreus mu-con
33	260	61.9	76	23	ABB88273	C radiatus mu-cono
34	259	61.7	75	23	ABB88228	C lynceus mu-conop
35	258.5	61.5	70	23	ABB88153	C bandanus mu-cono
36	255.5	60.8	74	23	ABB88171	C bullatus mu-cono
37	255	60.7	71	23	ABB88218	C laterculatus mu-
38	252	60.0	68	23	ABB88263	C pulicarius mu-co
39	252	60.0	75	23	ABB88271	C radiatus mu-cono
40	250.5	59.6	74	23	ABB88145	C aurisilacus mu-co
41	250.5	59.6	74	23	ABB88392	C consors mu-conop
42	250	59.5	65	23	ABB88216	C laterculatus mu-
43	250	59.5	74	23	ABB88222	C marmoreus mu-con
44	249.5	59.4	69	23	ABB88246	C bullatus mu-cono
45	249.5	59.4	74	23	ABB88173	

ALIGNMENTS

RESULT 1
ABB88283
ID ABB88283 standard; Protein: 75 AA.
XX ABB88283;
XX AC
XX AC
XX 24-MAY-2002 (first entry)
DT
DT
DE C striatus mu-conopeptide S3-2 propeptide.
XX
XX Mu-conopeptide; snail; venom: voltage-gated sodium channel; analgesic;
KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
KW neurodegenerative disease; neuromuscular disorder.
XX
XX Conus striatus.
XX
XX WO200207678-A2.
PN
PN 31-JAN-2002.
PD
PD
XX 23-JUL-2001; 2001WO-US23125.
XX
XX 21-JUL-2000; 2000US-219619P.
PR 03-NOV-2000; 2000US-245157P.
PR 29-JAN-2001; 2001US-264319P.
PR 21-MAR-2001; 2001US-277270P.
XX
XX (UTAH) UNIV UTAH RES FOUND.
PA (COGN-) COGNETIX INC.
XX
XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;

Fri Jan 10 09:33:17 2003

PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX WPI; 2002-217020/27.
 DR N-PSDB; ABL88549.
 DR

XX New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 PT

XX Claim 9; Page 56; 231pp; English.
 PS

XX The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC anyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide preprotein of the invention.
 CC

XX Sequence 75 AA;
 SQ

Query Match 100.0%; Score 420; DB 23; Length 75;
 Best Local Similarity 100.0%; Pred. No. 1.4e-40;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMSKGLVLTVCLLFPLTALPLDGDQPADRAERMQDDISSDEHPLFDKRONCCNG 60
 DB 1 GMSKGLVLTVCLLFPLTALPLDGDQPADRAERMQDDISSDEHPLFDKRONCCNG 60

QY 61 CSSKWCRRDHARCCGR 75
 DB 61 CSSKWCRRDHARCCGR 75

RESULT 2
 ID ABB88344
 XX ABB88344 standard; Protein; 76 AA.
 AC ABB88344;

XX 24-MAY-2002 (first entry)
 DT

XX C stercusmuscarum mu-conopeptide Sm3-3 propeptide.
 DE

XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.
 XX

OS Conus stercusmuscarum.
 XX

XX WO200207678-A2.
 PN

XX 31-JAN-2002.
 PD

XX 23-JUL-2001; 2001WO-US23125.
 PF

XX 21-JUL-2000; 2000US-219619P.
 PR

XX 03-NOV-2000; 2000US-245157P.
 PR

XX 29-JAN-2001; 2001US-264319P.
 PR

XX 21-MAR-2001; 2001US-277270P.
 PR

XX (UTAH) UNIV UTAH RES FOUND.
 PA

XX (COGN-) COGNETIX INC.
 PA

PI Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 XX Jacobsen R, Jones RM, Cartier GE, Shen GS;
 DR WPI; 2002-217020/27.
 DR N-PSDB; ABL88578.
 DR

XX New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 PT

XX Claim 9; Page 69; 231pp; English.
 PS

XX The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC anyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide preprotein of the invention.
 CC

XX Sequence 76 AA;
 SQ

Query Match 88.6%; Score 372; DB 23; Length 76;
 Best Local Similarity 88.0%; Pred. No. 4.4e-35;
 Matches 66; Conservative 5; Mismatches 2; Indels 2; Gaps 1;

QY 3 MMSKGLVLTVCLLFPLTALPLDGDQPADRAERMQDDISSDEHPLFDKRONCCNG--G 60
 DB 1 MMSKGLVLTVCLLFPLTALPLDGDQPADRAERMQDDISSDEHPLFDKRONCCNGRG 60

QY 61 CSSKWCRRDHARCCGR 75
 DB 61 CSSKWCRRDHARCCGR 75

RESULT 3
 ID ABB88394
 XX ABB88394 standard; Protein; 74 AA.
 AC ABB88394;

XX 24-MAY-2002 (first entry)
 DT

XX C consors mu-conopeptide Cn3-3 propeptide.
 DE

XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.
 XX

OS Conus consors.
 XX

XX WO200207678-A2.
 PN

XX 31-JAN-2002.
 PD

XX 23-JUL-2001; 2001WO-US23125.
 PF

XX 21-JUL-2000; 2000US-219619P.
 PR

XX 03-NOV-2000; 2000US-245157P.
 PR

XX 29-JAN-2001; 2001US-264319P.
 PR

XX 21-MAR-2001; 2001US-277270P.
 PR

XX (UTAH) UNIV UTAH RES FOUND.
 PA

XX (COGN-) COGNETIX INC.
 PA

XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX WPI: 2002-217020/27.
 DR N-PSDB; ABL88603.
 XX
 PT New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 XX
 PS Claim 9; Page 80; 231pp; English.
 XX
 CC The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide preprotein of the invention.
 XX
 SQ Sequence 74 AA;
 Query Match 79.8%; Score 335; DB 23; Length 74;
 Best Local Similarity 79.7%; Pred. No. 7.3e-31;
 Matches 59; Conservative 6; Mismatches 7; Indels 2; Gaps 1;
 QY 3 MMSKLGVLTVCLLLPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRNCCN--GG 60
 Db 1 MMSKLGVLTVCLLLPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRNCCN--GG 60
 QY 61 CSSKWCRCRDHARCCG 74
 Db 61 CSGRWCRCRDHARCCG 74
 RESULT 4
 ID ABB88167
 XX ABB88167 standard; Protein; 80 AA.
 XX
 AC ABB88167;
 XX
 DT 24-MAY-2002 (first entry)
 XX
 DE C bullatus mu-conopeptide Bu3-3 propeptide.
 XX
 KW Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.
 XX
 OS Conus bullatus.
 XX
 PN WO200207678-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 23-JUL-2001; 2001WO-US23125.
 XX
 PR 21-JUL-2000; 2000US-219619P.
 PR 03-NOV-2000; 2000US-245157P.
 PR 29-JAN-2001; 2001US-264319P.
 PR 21-MAR-2001; 2001US-277270P.
 XX
 XX (UTAH) UNIV UTAH RES FOUND.

PA (COGN-) COGNETIX INC.
 XX
 PI Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX WPI: 2002-217020/27.
 DR N-PSDB; ABL88496.
 XX
 PT New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 XX
 PS Claim 9; Page 29; 231pp; English.
 XX
 CC The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide preprotein of the invention.
 XX
 SQ Sequence 80 AA;
 Query Match 76.2%; Score 320; DB 23; Length 80;
 Best Local Similarity 75.0%; Pred. No. 4.1e-29;
 Matches 60; Conservative 7; Mismatches 5; Indels 8; Gaps 3;
 QY 3 MMSKLGVLTVCLLLPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKR--QNCCN-- 58
 Db 1 MMSKLGVLTVCLLLPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKR--QNCCN-- 58
 QY 59 ---GGCSSKWCRCRDHARCCG 75
 Db 61 NGKRCG-SRWCRDHSRCCG 79
 RESULT 5
 ID ABB88396
 XX ABB88396 standard; Protein; 76 AA.
 XX
 AC ABB88396;
 XX
 DT 24-MAY-2002 (first entry)
 XX
 DE C consors mu-conopeptide Cn3-4 propeptide.
 XX
 KW Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.
 XX
 OS Conus consors.
 XX
 PN WO200207678-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 23-JUL-2001; 2001WO-US23125.
 XX
 PR 21-JUL-2000; 2000US-219619P.
 PR 03-NOV-2000; 2000US-245157P.
 PR 29-JAN-2001; 2001US-264319P.
 PR 21-MAR-2001; 2001US-277270P.
 XX

(UTAH) UNIV UTAH RES FOUND.
(COGN-) COGNETIX INC.

Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
Jacobsen R, Jones RM, Cartier GE, Shen GS;

WPI; 2002-217020/27.
N-PSDB; ABL88604.

New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as neuroprotective agents

Claim 9; Page 80; 231pp; English.

The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.

Query Match 73.0%; Score 306.5; DB 23; Length 76;
Best Local Similarity 76.3%; Pred. No. 1.3e-27;
Matches 58; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

3 MMSKLGVLTVCLLLPLTALPDGQDPADPAPERMQDDISSDEHPLFDKRONCC---NG 59
1 MMSKLGVLTVCLLLPLTALPDGQDPADPAPERMQDDISSDEHPLFDKRONCCGKG 60

60 GCSKMKCRDHARCCGR 75
61 SCGKACKSLKCCSGR 76

RESULT 6
ABB88165
ID ABB88165 standard; Protein; 78 AA.
AC ABB88165;
DT 24-MAY-2002 (first entry)
DE C bullatus mu-conopeptide Bu3-2 propeptide.
XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
KW neurodegenerative disease; neuromuscular disorder.
XX Conus bullatus.
OS
XX WO200207678-A2.
PN
XX 31-JAN-2002.
PD
XX 23-JUL-2001; 2001WO-US23125.
PF
XX 21-JUL-2000; 2000US-219619P.
PR
XX 03-NOV-2000; 2000US-245157P.
PR
XX 29-JAN-2001; 2001US-264319P.
PR
XX 21-MAR-2001; 2001US-277270P.

(UTAH) UNIV UTAH RES FOUND.
(COGN-) COGNETIX INC.

Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
Jacobsen R, Jones RM, Cartier GE, Shen GS;

WPI; 2002-217020/27.
N-PSDB; ABL88495.

New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as neuroprotective agents

Claim 9; Page 29; 231pp; English.

The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide preprotein of the invention.

Query Match 72.9%; Score 306; DB 23; Length 78;
Best Local Similarity 75.6%; Pred. No. 1.6e-27;
Matches 59; Conservative 8; Mismatches 5; Indels 6; Gaps 4;

3 MMSKLGVLTVCLLLPLTALPDGQDPADPAPERMQDDISSDEHPLFDKR--QNCC-NG 59
1 MMSKLGVLTVCLLLPLTALPDGQDPADPAPERMQDDISSQNPLLEKRVGERCKNG 60

60 --GCSKMKCRDHARCCGR 75
61 KRGC-GRWCRDHSRCCGR 77

RESULT 7
ABB88318
ID ABB88318 standard; Protein; 75 AA.
XX ABB88318;
AC ABB88318;
DT 24-MAY-2002 (first entry)
DE C tulipa mu-conopeptide T3-2 propeptide.
XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
KW neurodegenerative disease; neuromuscular disorder.
XX Conus tulipa.
OS
XX WO200207678-A2.
PN
XX 31-JAN-2002.
PD
XX 23-JUL-2001; 2001WO-US23125.
PF
XX 21-JUL-2000; 2000US-219619P.
PR
XX 03-NOV-2000; 2000US-245157P.
PR
XX 29-JAN-2001; 2001US-264319P.

PR 21-MAR-2001; 2001US-277270P.
XX (UTAH) UNIV UTAH RES FOUND.
PA (COGN-) COGNEX INC.
XX
PI Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
XX
DR WPI; 2002-217020/27.
DR N-PSDB; ABL88566.
XX
XX New mu-conopeptides useful for treating disorders associated with
PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
PT blocking agents, as local anesthetic agents, as analgesic agents and as
PT neuroprotective agents
XX
XX Claim 9; Page 64; 23lpp; English.
XX
CC The present invention relates to mu-conopeptides derived from snails,
CC which can be in the treatment of disorders associated with voltage-gated
CC ion channels. These may include neurodegenerative disorders such as
CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
CC or ischaemia which typically follows stroke, cerebrovascular accident,
CC brain or spinal cord trauma, myocardial infarct, physical trauma,
CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
CC providing muscle relaxation, treating essential blepharospasm and other
CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
CC is a mu-conopeptide preprotein of the invention.
XX
XX Sequence 75 AA;
XX
Query Match 72.5%; Score 304.5; DB 23; Length 75;
Best Local Similarity 74.7%; Pred. No. 2.3e-27;
Matches 56; Conservative 9; Mismatches 7; Indels 3; Gaps 2;
QY 3 MMSKLGVLTVCLLPLTALPLDGDQPADRPAERMDDISSDEHPLFDKRONCCNG--G 60
DB 1 MMSKLGVLTVCLLPLTALPLDGDQPADRPAERMDDISSDEHPLFDKRONCCNG--G 60
QY 61 CSSKRCRQ-HCCGR 75
DB 61 CSSKRCRQ-HCCGR 74
RESULT 8
ABB88149
ID ABB88149 standard; Protein: 78 AA.
XX
AC ABB88149;
XX
XX 24-MAY-2002 (first entry)
XX
XX C aurisiacus mu-conopeptide A3-3 propeptide.
XX
XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
XX anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
XX cerebroprotective; anticonvulsant; antitachycardic; antidiabetic;
XX cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
XX neurodegenerative disease; neuromuscular disorder.
XX
XX Conus aurisiacus.
XX
XX WO200207678-A2.
XX
XX 31-JAN-2002.
XX
XX 23-JUL-2001; 2001WO-US23125.
XX
XX 21-JUL-2000; 2000US-219619P.
XX
XX 03-NOV-2000; 2000US-245157P.

PR 29-JAN-2001; 2001US-264319P.
PR 21-MAR-2001; 2001US-277270P.
XX
XX (UTAH) UNIV UTAH RES FOUND.
PA (COGN-) COGNEX INC.
XX
XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
XX
XX WPI; 2002-217020/27.
DR N-PSDB; ABL88487.
XX
XX New mu-conopeptides useful for treating disorders associated with
PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
PT blocking agents, as local anesthetic agents, as analgesic agents and as
PT neuroprotective agents
XX
XX Claim 9; Page 25; 23lpp; English.
XX
CC The present invention relates to mu-conopeptides derived from snails,
CC which can be in the treatment of disorders associated with voltage-gated
CC ion channels. These may include neurodegenerative disorders such as
CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
CC or ischaemia which typically follows stroke, cerebrovascular accident,
CC brain or spinal cord trauma, myocardial infarct, physical trauma,
CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
CC providing muscle relaxation, treating essential blepharospasm and other
CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
CC is a mu-conopeptide preprotein of the invention.
XX
XX Sequence 78 AA;
XX
Query Match 72.3%; Score 303.5; DB 23; Length 78;
Best Local Similarity 71.8%; Pred. No. 3.1e-27;
Matches 56; Conservative 9; Mismatches 10; Indels 3; Gaps 1;
QY 1 GSMMSKLGVLTVCLLPLTALPLDGDQPADRPAERMDDISSDEHPLFDKRONCC--- 57
DB 1 GSMMSKLGVLTVCLLPLTALPLDGDQPADRPAERMDDISSDEHPLFDKRONCCCTGK 60
QY 58 NGGCSKRCRDHARCCGR 75
DB 61 KGCSGSKACKNLKCCGR 78
RESULT 9
ABB88261
ID ABB88261 standard; Protein: 78 AA.
XX
AC ABB88261;
XX
XX 24-MAY-2002 (first entry)
XX
XX C nobilis mu-conopeptide NB3-2 propeptide.
XX
XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
XX anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
XX cerebroprotective; anticonvulsant; antitachycardic; antidiabetic;
XX cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
XX neurodegenerative disease; neuromuscular disorder.
XX
XX Conus nobilis.
XX
XX WO200207678-A2.
XX
XX 31-JAN-2002.
XX
XX 23-JUL-2001; 2001WO-US23125.
XX
XX 21-JUL-2000; 2000US-219619P.

PR 03-NOV-2000; 2000US-245157P.
 PR 29-JAN-2001; 2001US-264319P.
 PR 21-MAR-2001; 2001US-277270P.
 XX
 XX (UTAH) UNIV UTAH RES FOUND.
 XX (COGN-) COGNETIX INC.

XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX
 XX WPI: 2002-217020/27.
 DR N-PSDB; ABL88539.

XX New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 XX

PS Claim 9; Page 51; 231pp; English.

XX The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide preprotein of the invention.
 XX

SQ Sequence 78 AA;

Query Match 72.3%; Score 303.5; DB 23; Length 78;
 Best Local Similarity 71.8%; Pred. No. 3.1e-27;
 Matches 56; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

Qy 1 GSMSKGLVLTICLLLPALTALPDGQADPAPERMQDDISSDEHPLFDKRNCC-- 57

Db 1 GSMSKGLVLTICLLLPALTALPDGQADPAPERMQDDISSDEHPLFDKRNCCCTGK 60

Qy 58 NGGSSKWCGRDHARCCGR 75

Db 61 KGSCSGKACKNLKCCSGR 78

RESULT 10
 ABB88299
 ID ABB88299 standard; Protein; 74 AA.

XX AC ABB88299;

XX DT 24-MAY-2002 (first entry)

XX DE C tulipa mu-conopeptide T3-1 propeptide.

XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.

XX OS Conus tulipa.

XX XX WO200207678-A2.

XX XX 31-JAN-2002.

XX XX 23-JUL-2001; 2001WO-US23125.

XX PF

PR 21-JUL-2000; 2000US-219619P.
 PR 03-NOV-2000; 2000US-245157P.
 PR 29-JAN-2001; 2001US-264319P.
 PR 21-MAR-2001; 2001US-277270P.

XX (UTAH) UNIV UTAH RES FOUND.
 XX (COGN-) COGNETIX INC.

XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX

XX WPI: 2002-217020/27.
 DR N-PSDB; ABL88537.

XX New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 XX

PS Claim 9; Page 60; 231pp; English.

XX The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide preprotein of the invention.
 XX

SQ Sequence 74 AA;

Query Match 71.3%; Score 299.5; DB 23; Length 74;
 Best Local Similarity 74.3%; Pred. No. 8.3e-27;
 Matches 55; Conservative 9; Mismatches 7; Indels 3; Gaps 2;

Qy 4 MSKLGVLITVCLLLPALTALPDGQADPAPERMQDDISSDEHPLFDKRNCCNG--GC 61

Db 1 MSKLGVLITICLLLPALTALPDGQADPAPERMQDDISSDEHPLFDKRNCCNGGEC 60

Qy 62 SSKWCGRDHARCCGR 75

Db 61 SSRECRPQ-HCCGR 73

RESULT 11
 ABB88163
 ID ABB88163 standard; Protein; 77 AA.

XX AC ABB88163;

XX DT 24-MAY-2002 (first entry)

XX DE C bullatus mu-conopeptide Bu3-1A propeptide.

XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.

XX OS Conus bullatus.

XX XX WO200207678-A2.

XX XX 31-JAN-2002.

XX XX 23-JUL-2001; 2001WO-US23125.

XX PF

XX 21-JUL-2000; 2000US-219619P.
 PR 03-NOV-2000; 2000US-245157P.
 PR 29-JAN-2001; 2001US-264319P.
 PR 21-MAR-2001; 2001US-277270P.
 XX (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX WPI: 2002-217020/27.
 DR N-PSDB; ABL88494.
 XX
 PT New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 XX
 PS Claim 9; Page 28; 231pp; English.
 XX
 CC The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide preprotein of the invention.
 XX Sequence 77 AA;
 SQ
 Query Match 71.3%; Score 299.5; DB 23; Length 77;
 Best Local Similarity 74.0%; Pred. No. 8.6e-27;
 Matches 57; Conservative 7; Mismatches 8; Indels 5; Gaps 3;
 QY 3 MMSKLGVLTVCLLLPPLTALPLDQPADRPAERMQDDISSDEHPLFDKR--QNCNG- 59
 DB 1 MMSKLGVLTVCLLLPPLTALPLDQPADRPAERMQDDISSDEHPLFDKR--QNCNG- 59
 QY 60 -GCSSKWCGRDHARCCGR 75
 DB 61 RGC-GRWCGRDHARCCGR 76
 RESULT 12
 ABB88320
 ID ABB88320 standard; Protein; 76 AA.
 AC ABB88320;
 XX
 XX 24-MAY-2002 (first entry)
 DT
 DE C aurisiacus mu-conopeptide A3-5 propeptide.
 XX
 KW Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antitoxic; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.
 XX
 OS Conus aurisiacus.
 XX
 XX W0200207678-A2.
 PN
 XX 31-JAN-2002.
 PD
 XX

PF 23-JUL-2001; 2001WO-US23125.
 XX
 PR 21-JUL-2000; 2000US-219619P.
 PR 03-NOV-2000; 2000US-245157P.
 PR 29-JAN-2001; 2001US-264319P.
 PR 21-MAR-2001; 2001US-277270P.
 XX (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX WPI: 2002-217020/27.
 DR N-PSDB; ABL88567.
 XX
 PT New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 XX
 PS Claim 9; Page 64; 231pp; English.
 XX
 CC The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide preprotein of the invention.
 XX Sequence 76 AA;
 SQ
 Query Match 69.9%; Score 293.5; DB 23; Length 76;
 Best Local Similarity 71.1%; Pred. No. 4.1e-26;
 Matches 54; Conservative 9; Mismatches 10; Indels 3; Gaps 1;
 QY 3 MMSKLGVLTVCLLLPPLTALPLDQPADRPAERMQDDISSDEHPLFDKRQNC- 59
 DB 1 MMSKLGVLTVCLLLPPLTALPLDQPADRPAERMQDDISSDEHPLFDKRQNC- 59
 QY 60 GCSSKWCGRDHARCCGR 75
 DB 61 SCSSKACKNLKCCGR 76
 RESULT 13
 ABB88277
 ID ABB88277 standard; Protein; 75 AA.
 AC ABB88277;
 XX
 XX 24-MAY-2002 (first entry)
 DT
 DE C stercusmuscarum mu-conopeptide Sm3-1 propeptide.
 XX
 KW Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antitoxic; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.
 XX
 OS Conus stercusmuscarum.
 XX
 XX W0200207678-A2.
 PN
 XX 31-JAN-2002.
 PD

XX PF 23-JUL-2001; 2001WO-US23125.
 XX PR 21-JUL-2000; 2000US-219619P.
 XX PR 03-NOV-2000; 2000US-245157P.
 XX PR 29-JAN-2001; 2001US-264319P.
 XX PR 21-MAR-2001; 2001US-277270P.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PA (COGN-) COGNETIX INC.
 XX XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 XX PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX XX WPI: 2002-217020/27.
 XX DR N-PSDB; ABL88546.
 XX XX New mu-conopeptides useful for treating disorders associated with
 XX PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 XX PT blocking agents, as local anesthetic agents, as analgesic agents and as
 XX PT neuroprotective agents -
 XX XX Claim 9; Page 54; 231pp; English.
 XX XX The present invention relates to mu-conopeptides derived from snails,
 XX CC which can be in the treatment of disorders associated with voltage-gated
 XX CC ion channels. These may include neurodegenerative disorders such as
 XX CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 XX CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 XX CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 XX CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 XX CC or ischaemia which typically follows stroke, cerebrovascular accident,
 XX CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 XX CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 XX CC providing muscle relaxation, treating essential blepharospasm and other
 XX CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 XX CC is a mu-conopeptide preprotein of the invention.
 XX SQ Sequence 75 AA;
 Query Match 69.6%; Score 292.5; DB 23; Length 75;
 Best Local Similarity 72.0%; Pred. No. 5.3e-26;
 Matches 54; Conservative 9; Mismatches 9; Indels 3; Gaps 1;
 QY 4 MSKGLVLTVCLLPLTALPLDGDQPADRAERMQDDISSEHPLEDKRQNC---NGG 60
 Db 1 MSKGLVLTICLLPLTALPLDGDQPADQADRMQDDISSEQVPLFDKQKCKCTGKKGS 60
 QY 61 CSSKWCRRHARCCGR 75
 Db 61 CSGKACKNLKCCSGR 75
 RESULT 14
 ABB88161
 ID ABB88161 standard; Protein; 77 AA.
 XX AC ABB88161;
 XX XX 24-MAY-2002 (first entry)
 XX DE C bullatus mu-conopeptide Bu3-1 propeptide.
 XX KW Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antitoxic; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.
 XX OS Conus bullatus.
 XX PN WO200207678-A2.
 XX XX

PD 31-JAN-2002.
 XX PF 23-JUL-2001; 2001WO-US23125.
 XX PR 21-JUL-2000; 2000US-219619P.
 XX PR 03-NOV-2000; 2000US-245157P.
 XX PR 29-JAN-2001; 2001US-264319P.
 XX PR 21-MAR-2001; 2001US-277270P.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PA (COGN-) COGNETIX INC.
 XX XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 XX PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX XX WPI: 2002-217020/27.
 XX DR N-PSDB; ABL88493.
 XX XX New mu-conopeptides useful for treating disorders associated with
 XX PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 XX PT blocking agents, as local anesthetic agents, as analgesic agents and as
 XX PT neuroprotective agents -
 XX XX Claim 9; Page 28; 231pp; English.
 XX XX The present invention relates to mu-conopeptides derived from snails,
 XX CC which can be in the treatment of disorders associated with voltage-gated
 XX CC ion channels. These may include neurodegenerative disorders such as
 XX CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 XX CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 XX CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 XX CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 XX CC or ischaemia which typically follows stroke, cerebrovascular accident,
 XX CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 XX CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 XX CC providing muscle relaxation, treating essential blepharospasm and other
 XX CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 XX CC is a mu-conopeptide preprotein of the invention.
 XX SQ Sequence 77 AA;
 Query Match 69.6%; Score 292.5; DB 23; Length 77;
 Best Local Similarity 72.7%; Pred. No. 5.4e-26;
 Matches 56; Conservative 7; Mismatches 9; Indels 5; Gaps 3;
 QY 3 MMSKGLVLTVCLLPLTALPLDGDQPADRAERMQDDISSEHPLEDKR-QNCCNG- 59
 Db 1 MMSKGLVLTICLLPLTALPLDGDQPADRAERMQDDISSEQNSLLEKRVTDRCCKG 60
 QY 60 -GCSSKWCRRHARCCGR 75
 Db 61 REC-GRWCRDHSRCCGR 76
 RESULT 15
 ABB88238
 ID ABB88238 standard; Protein; 74 AA.
 XX AC ABB88238;
 XX XX 24-MAY-2002 (first entry)
 XX DE C magus mu-conopeptide M3-5 propeptide.
 XX KW Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antitoxic; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.
 XX OS Conus magus.
 XX PN WO200207678-A2.



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OM protein - protein search, using sw model

Run on: January 10, 2003, 08:32:32 ; Search time 24.1304 Seconds
(without alignments)
298.796 Million cell updates/sec

Title: US-09-910-009A-210

Perfect score: 420

Sequence: 1 GSMMSKLGVLVLCVLLFFPL.....CCNGGSSKWCARDHARCCGR 75

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71.5	17.0	63	2 A58511	bromocontryphan pr
2	69.5	15.9	2	C83305	hypothetical prote
3	68.5	16.3	206	2 JS0646	22k antifungal pro
4	68.5	16.3	227	2 T02075	antifungal zeamati
5	65.5	15.6	206	2 A25581	alpha-amylase/tryp
6	64.5	15.4	316	2 S07569	protein H5 - slime
7	64	15.2	71	2 S41614	high-potential iro
8	64	15.2	203	2 H69937	hypothetical prote
9	64	15.2	405	2 H69711	mutants block spor
10	64	15.2	644	2 JC5119	anti-mullerian hor
11	63.5	15.1	839	2 H87561	sensor histidine k
12	63	15.0	93	2 A09060	hypothetical prote
13	63	15.0	130	2 B85808	unknown protein en
14	63	15.0	134	1 WTBO	seminal fluid prot
15	63	15.0	523	2 T22484	hypothetical prote
16	62.5	14.9	957	2 S44748	C06G4.1 protein -
17	62	14.8	880	2 S61908	DNA-binding protei
18	62	14.8	1115	2 S04241	G protein-coupled
19	61	14.5	602	2 H86468	protein F12K21.20
20	61	14.5	2591	2 T30288	pristinamycin I sy
21	60.5	14.4	160	2 D84023	hypothetical prote
22	60.5	14.4	346	2 JA0159	cysteine proteinas
23	60.5	14.4	466	2 T06416	cysteine proteinas
24	60.5	14.4	591	2 I48141	acroganin - guine
25	60	14.3	579	2 A42617	66k rel-related pr
26	59.5	14.2	90	2 T29013	hypothetical prote
27	59.5	14.2	157	2 A12936	conserved hypothet
28	59.5	14.2	159	2 F98345	hypothetical prote
29	59.5	14.2	324	2 C86582	hypothetical prote

30	59.5	14.2	324	2 D72041	conserved hypothet
31	59.5	14.2	385	2 A54785	preadipocyte facto
32	59.5	14.2	385	2 S53718	homeotic protein d
33	59.5	14.2	466	1 KFHU7	coagulation factor
34	59	14.0	152	2 S00332	alpha-amylase inh
35	59	14.0	219	2 T21736	hypothetical prote
36	59	14.0	263	2 A54648	hypothetical prote
37	59	14.0	680	2 S17982	stannocalcin prec
38	59	14.0	854	1 QRHYLD	Kallmann syndrome
39	58.5	13.9	125	2 S25454	LDL receptor precu
40	58.5	13.9	142	2 A71097	epididymis-specifi
41	58.5	13.9	274	2 S35339	hypothetical prote
42	58.5	13.9	443	2 I46932	trypsin (PC 3.4.21
43	58.5	13.9	452	2 T21728	coagulation factor
44	58.5	13.9	464	2 S24602	hypothetical prote
45	58.5	13.9	558	2 S58226	cysteine proteinas
					nodu protein - Rhi

ALIGNMENTS

RESULT 1

A58511

bromocontryphan precursor - cone shell (Conus radiatus)

N:Contains: contryphan: des-Gly-contryphan

C:Species: Conus radiatus (radial cone)

C>Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 07-May-1999

C:Accession: A58511; B58511; A43097

R:Jimenez, E.C.; Craig, A.G.; Watkins, M.; Hillyard, D.R.; Gray, W.R.; Gulyas, J.; Ri

Biochemistry 36, 989-994, 1997

A:Title: Bromocontryphan: post-translational bromination of tryptophan.

A:Reference number: A58511; MUID:97185706; PMID:9033387

A:Accession: A58511

A:Molecule type: mRNA

A:Residues: 1-63 <JIM1>

A:Accession: B58511

A:Molecule type: Protein

A:Residues: 55-62 <JIM2>

R:Jimenez, E.C.; Olivera, B.M.; Gray, W.R.; Cruz, L.J.

J. Biol. Chem. 271, 28002-28005, 1996

A:Title: Contryphan is a D-tryptophan-containing Conus peptide.

A:Reference number: A43097; MUID:97067006; PMID:8910408

A:Accession: A43097

A:Molecule type: Protein

A:Residues: 55-62 <JIM3>

A:Experimental source: Venom

C:Superfamily: unassigned conotoxins

C:Keywords: amidated carboxyl end; bromine; D-amino acid; hydroxyproline; toxin; veno

F:55-62/Product: contryphan #status experimental <MAT1>

F:56-62/Product: bromocontryphan #status experimental <MAT2>

F:56-62/Dissulfide bonds: #status experimental

F:57/Modified site: 4-hydroxyproline (Pro) #status experimental

F:58/Modified site: D-tryptophan (Trp) #status experimental

F:61/Modified site: 6-bromotryptophan (Trp) #link MAT2 #status experimental

F:62/Modified site: amidated carboxyl end (Cys) (amide in mature form from following

Query Match 17.0%; Score 71.5; DB 2; Length 63;

Best Local Similarity 30.8%; Pred. No. 0.91;

Matches 24; Conservative 6; Mismatches 17; Indels 31; Gaps 4;

QY 4 MSKLGVLVLTVCVLLFFPLTALPLDQPADRPAPERMDDISSDEHPLFDKQNCNGGCS 62

Db 1 MGKTLILVLAVALLSAQVVGDDQPADRNA-----VPRDDNP-----GCAS 44

QY 63 SK-----WC 66

Db 45 GKFNWLRSSGCPWEPWC 62

RESULT 2

C83305

hypothetical protein PA2721 [imported] - Pseudomonas aeruginosa (strain PA01)

A;Status: preliminary

A; Molecule type: DNA

A;Residues: 1-134 <BR3>
A;Cross-references: EMBL:Z33621; NID:g488602; PIDN:CAA83915.1; PID:g488603
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994
R;Calvete, J.J.; Raida, M.; Sanz, L.; Wempe, F.; Scheit, K.H.; Romero, A.; Toepfer-Peter
FEBS Lett. 350, 203-206, 1994
A;Title: Localization and structural characterization of an oligosaccharide O-linked to
ated spermatozoa.

A;Reference number: S48674; MUID:94350099; PMID:8070564

A;Accession: S48674

A;Molecule type: protein

A;Residues: 26-35, 'X', 37-56; 60-89 <CAL>

C;Genetics:

A;Introns: 26/1; 46/1; 90/1

C;Superfamily: seminal fluid protein PDC-109; fibronectin type II repeat homology

C;Keywords: duplication; glycoprotein; plasma; semen

F;1-25/Domain: signal sequence #status predicted <SIG>

F;26-134/Product: seminal fluid protein SVSP109 #status experimental <MAT>

F;49-86/Domain: fibronectin type II repeat homology <2F0>

F;94-134/Domain: fibronectin type II repeat homology <2F1>

F;36/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental

F;49-73,63-86,94-119,108-134/Disulfide bonds: #status experimental

Query Match 15.0%; Score 63; DB 1; Length 134;

Best Local Similarity 25.5%; Pred. No. 13;

Matches 24; Conservative 11; Mismatches 35; Indels 24; Gaps 3;

QY 3 MMSKLGVLTVCLLPLTALPDGQPADRPARMOD---DISSDEHPLFD-----KR 53

Db 1 MALQLGLFLIAGVSVFLQLDPVNGDQGVSTPTQDGPALPEDECVFFPVYRNKH 60

QY 54 QNCCNGGCSKWC-----RDHARC 72

Db 61 FDCVTGSLFPMCSLDADYVGRWKYCAQRDYAKC 94

RESULT 15

T22484

hypothetical protein F52B11.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C;Accession: T22484

R;Matthews, L.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z19569

A;Accession: T22484

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-523 <WIL>

A;Cross-references: EMBL:Z82268; PIDN:CAB05197.1; GSPDB:GN00022; CESP:F52B11.1

A;Experimental source: clone F52B11

C;Genetics:

A;Gene: CFSP:F52B11.1

A;Map position: 4

A;Introns: 57/1; 151/3; 268/3; 372/2; 482/1

C;Superfamily: Caenorhabditis elegans hypothetical protein F52B11.1

Query Match 15.0%; Score 63; DB 2; Length 523;

Best Local Similarity 32.1%; Pred. No. 38;

Matches 17; Conservative 6; Mismatches 16; Indels 14; Gaps 3;

QY 29 QPADRPAERMQDDISSDEHPLFDKRNCCNGGC-----SSKWCARDHARCCGR 75

Db 139 QSADLRKRRTQLNAEPDKHP-----RQCLNPNCIYESRDSKYCDE---CGK 183

Search completed: January 10, 2003, 08:36:20

Job time : 26.1304 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: January 10, 2003, 08:32:27 ; Search time 12.3913 Seconds
(without alignments)
251.041 Million cell updates/sec

Title: US-09-910-009A-210
Perfect score: 420
Sequence: 1 GSMMSKLGVLTVCLLPFL.....CNGGCSKWCRCRHARCCGR 75

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	17.4	333	1 AMP IMPBA	O24006 i antimicro
2	72.5	17.3	64	1 CXAL_CONST	P15471 conus stria
3	71.5	17.0	63	1 COW_CONRA	P58786 conus radia
4	70.5	16.8	63	1 COWL_CONTE	Q9nda7 conus texti
5	70	16.7	27	1 CXM3_CONPU	P58925 conus purpu
6	68.5	16.3	63	1 COW3_CONTE	Q9nda5 conus texti
7	68.5	16.3	227	1 ZEAM_MAIZE	P33679 zea mays (m
8	65.5	15.6	206	1 IAT_MAIZE	P13867 zea mays (m
9	64.5	15.4	316	1 VSH5_DICDI	P14326 dictyosteli
10	64	15.2	71	1 HP12_ECTVA	P38524 ectothiorho
11	64	15.2	203	1 YFJP_BACSU	P54172 bacillus su
12	64	15.2	405	1 S3AE_BACSU	P49782 bacillus su
13	63	15.0	134	1 SPPL_BOVIN	P02784 bos taurus
14	62.5	14.9	63	1 COW2_CONTE	Q9nda5 conus texti
15	62.5	14.9	886	1 YRKL_CABEL	P34307 caenorhabdi
16	62	14.8	1115	1 GPCR_LYMST	P46023 lymnaea sta
17	61.5	14.6	63	1 COW_CONSE	P58787 conus sterc
18	60.5	14.4	346	1 COWL_CONTE	P20721 lycopersico
19	60.5	14.4	591	1 GRN_CAVPO	P28797 cavia porce
20	60	14.3	579	1 RELB_HUMAN	Q1201 homo sapien
21	59.5	14.2	324	1 Y734_CHLFP	Q927hl chlamydia p
22	59.5	14.2	385	1 DLK_MOUSE	Q09163 mus musculu
23	59.5	14.2	466	1 FA7_HUMAN	P08709 homo sapien
24	59	14.0	152	1 IAA2_HORVU	P13691 hordeum vul
25	59	14.0	250	1 SFC_LAGAU	P18301 anguilla au
26	59	14.0	274	1 TRYL_ANOGA	P35035 anopheles g
27	59	14.0	680	1 KALM_HUMAN	P23352 homo sapien
28	59	14.0	854	1 LBLR_CRIGR	P35950 cricetus
29	58.5	13.9	124	1 WFD2_HUMAN	Q14508 homo sapien
30	58.5	13.9	444	1 FA7_RABIT	P98139 oryctolagus
31	58.5	13.9	452	1 YOX4_CABEL	Q09317 caenorhabdi
32	58.5	13.9	558	1 NODU_RHISN	P13957 rhizobium s
33	58	13.8	123	1 WFD2_RABIT	Q28631 oryctolagus

P70375 mus musculu
Q92574 homo sapien
Q9hfy6 blastoclad
P46770 echinococcu
P26710 african swi
Q14596 homo sapien
P23137 nicotiana t
P49795 homo sapien
O00214 homo sapien
P00735 bos taurus
P10247 rattus norv
P23623 neurospora

ALIGNMENTS

RESULT 1	AMP_IMPBA	STANDARD:	PRT:	333 AA.
AC	O24006:			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Antimicrobial peptides precursor (IB-AMP) [Contains: Basic peptide			
DE	AMP3 (IB-AMP3); Basic peptide AMP1-1 (IB-AMP1-1); Basic peptide AMP1-2			
DE	(IB-AMP1-2); Basic peptide AMP1-3 (IB-AMP1-3); Basic peptide AMP2 (IB-			
DE	AMP2); Basic peptide AMP4 (IB-AMP4)]			
GN	AMP.			
OS	Impatiens balsamina (Balsam).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Asteridae; Ericales; Balsaminaceae; Impatiens.			
OX	NCBI_TaxID=63779;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUP=Seed:			
RC	MEDLINE=97450977; PubMed=9305910;			
RA	Taylor R.H., Acland D.P., Attenborough S., Cammue B.P.A., Evans I.J.,			
RT	Osborn R.W., Ray J.A., Rees S.B., Broekaert W.F.;			
RT	"A novel family of small cysteine-rich antimicrobial peptides from			
RL	seed of Impatiens balsamina is derived from a single precursor			
RL	protein.";			
RP	J. Biol. Chem. 272:24480-24487(1997).			
RN	[2]			
RP	STRUCTURE BY NMR OF IB-AMP1.			
RX	MEDLINE=98128575; PubMed=9454586;			
RA	Patel S.U., Osborn R.W., Rees S.B., Thornton J.M.;			
RT	"Structural studies of Impatiens balsamina antimicrobial protein (IB-			
RT	AMP1).";			
RL	Biochemistry 37:983-990(1998).			
CC	-!- FUNCTION: PLAY A ROLE IN THE DEFENSE OF THE GERMINATING SEED			
CC	AGAINST MICRO-ORGANISMS, BY INHIBITING THE GROWTH OF A RANGE OF			
CC	FILAMENTOUS FUNGI AND BACTERIA, ESPECIALLY GRAM-POSITIVE BACTERIA.			
CC	NOT CYTOTOXIC FOR CULTURED HUMAN CELLS AND ARE THE SMALLEST KNOWN			
CC	PLANT-DERIVED ANTIMICROBIAL PEPTIDES. PEPTIDE IB-AMP4 HAS A HIGHER			
CC	ANTIFUNGAL ACTIVITY THAN IB-AMP1.			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN DRY MATURE SEED AND BY			
CC	THE STAGES 2-5 OF DEVELOPING SEED. THE PEPTIDE IB-AMP1 IS ALSO			
CC	DETECTED AT EARLY STAGES OF GERMINATION (24H AND 48H			
CC	POSTGERMINATION).			
CC	-!- DOMAIN: CONTAINS REPEATED ALTERNATING BASIC MATURE PEPTIDE AND			
CC	ACIDIC PROPEPTIDE DOMAINS.			
CC	-!- PTM: THE N-TERMINAL OF ALL PEPTIDES ARE BLOCKED. THE 4 CYSTEINE			
CC	RESIDUES IN ALL PEPTIDES ARE INVOLVED IN INTRACHAIN DISULFIDE			
CC	BONDS.			
CC	-!- MASS SPECTROMETRY: MW=2536.6; METHOD=Electrospray; RANGE=55-74.			
CC	-!- MASS SPECTROMETRY: MW=2464.6; METHOD=Electrospray; RANGE=103-122.			
CC	-!- MASS SPECTROMETRY: MW=2527.4; METHOD=Electrospray; RANGE=233-252.			
CC	-!- MASS SPECTROMETRY: MW=2522.6; METHOD=Electrospray; RANGE=279-298.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			

RESULT 3	
COW_CONRA	
ID	COW_CONRA STANDARD; PRT; 63 AA.
AC	P58786;
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Contryphan precursor [Contains: Contryphan-R (Bromocontryphan); [des- Gly1]Contryphan-R].
DE	Conus radiatus (Rayed cone).
OS	Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC	Neogastropoda; Conoidea; Conidae; Conus.
OX	NCBI_TaxID=61198;
RN	[1]
RP	SEQUENCE FROM N.A. SEQUENCE OF 55-62, SYNTHESIS OF BROMOCONTRYPHAN, AND MASS SPECTROMETRY.
RP	TISSUE=Venom duct, and Venom:
RC	MEDLINE=97185706; PubMed=9033387;
RX	Jimenez E.C., Craig A.G., Watkins M., Hillyard D.R., Gray W.R.,
RA	Gulyas J., Rivter J.E., Cruz L.J., Olivera B.M.;
RA	"Bromocontryphan: post-translational bromination of tryptophan.";
RT	Biochemistry 36:989-994 (1997).
RN	[2]
RN	SEQUENCE OF 55-62, SYNTHESIS OF CONTRYPHAN, AND MASS SPECTROMETRY.
RP	TISSUE=Venom;
RC	MEDLINE=97067006; PubMed=8910408;
RX	Jimenez E.C., Olivera B.M., Gray W.R., Cruz L.J.;
RA	"Contryphan is a D-tryptophan-containing Conus peptide.";
RT	J. Biol. Chem. 271:28002-28005 (1996).
RN	[3]

PubMed=12006587;
RA Nielsen K.J., Watson M., Adams D.J., Hammarstrom A.K., Gage P.W.,
Hill J.M., Craik D.J., Thomas L., Adams D., Alewood P.F., Lewis R.J.;
RA "Solution structure of mu-conotoxin P11A, a preferential inhibitor of
RT persistent TRX-sensitive sodium channels.";
PL J. Biol. Chem. 277:0-0(2002).
CC -!- FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium
CC channel. This peptide causes flaccid paralysis in both mice and
CC fish. It blocks reversibly rat neuronal type II channels, whereas
CC it blocks irreversibly amphibian muscle Na+ channels (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- PW: Exists in two forms due to cis-trans isomerization at Hyp-8.
CC -!- Adopts a predominantly trans conformation (Probable).
CC -!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS. MU-TYPE
CC FAMILY.
KW Toxin; Neurotoxin; Sodium channel inhibitor; Hydroxylation; Amidation;
KW Cleavage on pair of basic residues.
FT NON_TER 1 3 PROBABLE.
FT PROPEP <1 3 MU-CONOTOXIN P11A.
FT PEPTIDE 4 25
FT DISULFID 7 19
FT DISULFID 8 24
FT DISULFID 14 25
FT MOD_RES 4 4
FT MOD_RES 11 11
FT MOD_RES 21 21
FT MOD_RES 25 25
FT MUTAGEN 17 17
FT SEQUENCE 27 AA; 3224 MW; F0E19F45BC97AC13 CRC64;
Query Match 16.7%; Score 70; DB 1; Length 27;
Best Local Similarity 50.0%; Pred. No. 0.19; Indels 4; Gaps 2;
Matches 14; Conservative 3; Mismatches 7;
QY 51 DKRQNCNG--GCSKWCGRDHARCCGR 75
DB 1 EKRQLCCGFPKSCRSRQCKPH-RCCGR 27
RESULT 6
ID COW3 CONTE STANDARD; PRT; 63 AA.
AC Q9NDA6:
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Leu-contryphan-Tx precursor.
OS Conus textile (Cloth-of-gold cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6494;
RN [1]
RP SEQUENCE FROM N.A., SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom duct;
RX MEDLINE=21065809; PubMed=11137539;
RA Jimenez E.C., Watkins M., Juszcak L.J., Cruz L.J., Olivera B.M.;
RA "Contryphans, from Conus textile venom ducts.";
RL Toxicon 39:803-808(2001).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=880.5; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC

DR EMBL; AF166324; AAF82244.1; -.
KW Toxin; D-amino acid; Amidation; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 55 BY SIMILARITY.
FT PEPTIDE 56 62 LEU-CONTRYPHAN-TX (BY SIMILARITY).
FT MOD_RES 58 58 D-AMINO ACID (BY SIMILARITY).
FT MOD_RES 62 62 AMIDATION (G-63 PROVIDE AMIDE GROUP) (BY
FT SIMILARITY).
SQ SEQUENCE 63 AA; 6678 MW; 2A910957B7E44BB1 CRC64;
Query Match 16.3%; Score 68.5; DB 1; Length 63;
Best Local Similarity 29.5%; Pred. No. 0.58;
Matches 23; Conservative 7; Mismatches 17; Indels 31; Gaps 4;
QY 4 MSKLGVL-LTVGCLLFLPTALFLDGDQPADRPAERMQDDISSDEHPLFDKRONCNGCS 62
DB 1 MGKLTLLVLAVALLSAQVMVGDDQPADRKA-----VPREDNP-----GGAS 44
QY 63 SK-----WC 66
DB 45 GKLMVDVLRPKKCVLPWC 62
RESULT 7
ID ZEAM_MAIZE STANDARD; PRT; 227 AA.
AC P33679;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Zeamatin precursor.
GN ZLP.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. B73; TISSUE=Seed;
RX MEDLINE=95148737; PubMed=7846159;
RA Malehorn D.E., Borgmeyer J.R., Smith C.E., Shah D.M.;
RA "Characterization and expression of an antifungal zeamatin-like
RT protein (Zlp) gene from Zea mays.";
RL Plant Physiol. 106:1471-1481(1994).
RN [2]
RP SEQUENCE OF 21-48.
RA Roberts W.K., Sellitrennikoff C.P.;
RA "Zeamatin, an antifungal protein from maize with membrane-
RT permeabilizing activity.";
RL J. Gen. Microbiol. 136:1771-1778(1990).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=96133724; PubMed=8548448;
RA Bataglia M.A., Monzingo A.F., Ernst S., Roberts W., Robertus J.D.;
RA "The crystal structure of the antifungal protein zeamatin, a member
RT of the thaumatin-like PR-5 protein family.";
RL Nat. Struct. Biol. 3:19-23(1996).
CC -!- FUNCTION: HAS ANTIFUNGAL ACTIVITY. INHIBITS CANDIDA ALBICANS AND
CC TRICHODERMA RESEI; MARGINAL INHIBITION OBSERVED AGAINST
CC ALTERNARIA SOLANI AND NEUROSPORA CRASSA.
CC -!- SIMILARITY: BELONGS TO THE THAUMATIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U06831; AAA92882.1; -.
DR PIR; A33174; A33174.

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FT  DISULFID  118  194  BY SIMILARITY.
FT  DISULFID  124  177  BY SIMILARITY.
FT  DISULFID  132  142  BY SIMILARITY.
FT  DISULFID  146  155  BY SIMILARITY.
FT  DISULFID  156  164  BY SIMILARITY.
FT  DISULFID  168  108  BY SIMILARITY.
FT  CONFLICT  108  164  Y -> M (IN REF. 2).
SQ  SEQUENCE  206 AA;  22075 MW;  6C73E1BACAE090DE CRC64;

Query Match      15.6%; Score 65.5; DB 1; Length 206;
Best Local Similarity 29.8%; Pred. No. 3.5;
Matches 17; Conservative 8; Mismatches 19; Indels 13; Gaps 2;

QY  19  PLTALPLDGDQPADR-----PGRMQDDISDEHPFLDKRQNCNGCCSS 63
      | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  107  PYSEFLP-DGSGGSRGPRCAVDYVNAARPAELRGDVGCVNACPFVKDEYCCVGSAA 162
      | : | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
VSH5_DICDI
ID  VSH5_DICDI  STANDARD;  PRT;  316 AA.
AC  P14326;
DT  01-JAN-1990 (Rel. 13, Created)
DT  01-JAN-1990 (Rel. 13, Last sequence update)
DE  01-FEB-1996 (Rel. 33, Last annotation update)
DE  Vegetative specific protein H5.
DE  C1NB OR H5.
OS  Dictyostellium discoideum (Slime mold).
OC  Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX  NCBI_TaxId=44589;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=AX3;
RA  Singleton C.K., Manning S.S., Ken R.;
RL  Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.
CC  !- DEVELOPMENTAL STAGE: THIS PROTEIN IS EXPRESSED IN GROWING
CC  CELLS AND DEACTIVATED UPON THE INITIATION OF DEVELOPMENT.
CC  !- SIMILARITY: BELONGS TO THE "GDGX" FAMILY OF LIPOLYTIC ENZYMES.
CC  -----
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CC  -----
CC  EMBL; X15387; CAA33445.1; -.
CC  PIR; S07569; S07569.
CC  DictyDb; DD01021; cinB.
CC  InterPro; IPR000379; Ser_estrs_site.
CC  Hydrolase.
CC  ACT_SITE 69 69 POTENTIAL.
CC  ACT_SITE 165 165 POTENTIAL.
CC  SEQUENCE 316 AA; 36053 MW; 876C87A360F3C936 CRC64;

Query Match      15.4%; Score 64.5; DB 1; Length 316;
Best Local Similarity 24.6%; Pred. No. 6.5;
Matches 17; Conservative 7; Mismatches 14; Indels 31; Gaps 3;

QY  15  LLLFPLTALPLDGDQPADRPAERMDDTSSDEHPFLDKRQNCNGGCSKWC----- 66
      | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  170  LVYYPIT-----DCNLKHHPIIDLRESINKG--SNKWCNHYTNND 208
      | : | | | | | | | | | | | | | | | | | | | | | | | | | |

QY  67  --RDHARC 73
      | | | |
Db  209  SERDEITCC 217

RESULT 10
ID  HP12_ECTVA  STANDARD;  PRT;  71 AA.
ID  HP12_ECTVA
CC  P38524;

```

Fri Jan 10 09:33:18 2003

01-OCT-1994 (Rel. 30, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)
 High potential iron-sulfur protein isozyme 2 (HiPIP 2).
 Ecotiorhodospira vacuolata.
 Bacteria; Proteobacteria; gamma subdivision; Ecotiorhodospiraceae;
 Ecotiorhodospira.
 NCBI_TaxID=1054;
 [1]
 SEQUENCE.
 STRAIN=beta-1 / DSM 2111;
 MEDLINE=94145107; PubMed=8311477;
 Ambler R.P., Meyer T.E., Kamen M.D.;
 "Amino acid sequences of two high-potential iron sulfur proteins
 (HiPIPs) from the moderately halophilic purple phototrophic bacterium
 Ecotiorhodospira vacuolata.";
 Arch. Biochem. Biophys. 308:78-81(1994).
 [2]
 X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 STRAIN=beta-1 / DSM 2111;
 MEDLINE=94162261; PubMed=8117708;
 Benning M.M., Meyer T.E., Rayment I., Holden H.M.;
 "Molecular structure of the oxidized high-potential iron-sulfur
 protein isolated from Ecotiorhodospira vacuolata.";
 Biochemistry 33:2476-2483(1994).
 [3]
 FUNCTION: SPECIFIC CLASS OF HIGH-REDOX-POTENTIAL 4FE-4S
 FERREDOXINS. FUNCTIONS IN ANAEROBIC ELECTRON TRANSPORT IN MOST
 PURPLE AND IN SOME OTHER PHOTOSYNTHETIC BACTERIA AND IN AT LEAST
 ONE GENUS (PARACOCCLUS) OF HALOPHILIC, DENITRIFYING BACTERIA.
 THE MIDPOINT REDOX POTENTIAL FOR THIS PROTEIN IS +150 MV.
 [4]
 SUBUNIT: HOMODIMER.
 SIMILARITY: BELONGS TO THE HIGH POTENTIAL IRON-SULFUR PROTEIN
 (HIPIP) FAMILY.
 PDB: 1HPI; 30-APR-94.
 InterPro: IPR000170; Hipot_ironsul.
 Pfam: PF01355; HiPIP; 1.
 PRINTS: PF00374; HIPPIFERDOXIN.
 PROSITE: PS00596; HiPIP; 1.
 Electron transport; Iron-sulfur; 4Fe-4S; 3D-structure.
 METAL 34 34 IRON-SULFUR (4FE-4S).
 METAL 37 37 IRON-SULFUR (4FE-4S).
 METAL 51 51 IRON-SULFUR (4FE-4S).
 METAL 65 65 IRON-SULFUR (4FE-4S).
 STRAND 2 3
 TURN 6 7
 HELIX 9 13
 TURN 14 15
 STRAND 17 17
 HELIX 20 22
 TURN 26 27
 TURN 30 31
 HELIX 34 36
 TURN 37 37
 STRAND 38 39
 TURN 40 40
 STRAND 43 44
 TURN 48 51
 STRAND 52 53
 TURN 55 56
 STRAND 57 60
 TURN 61 62
 STRAND 64 64
 TURN 66 67
 STRAND 70 70
 SEQUENCE 71 AA; 7819 MW; EE2FA335594898C7 CRC64;
 Query Match 15.2%; Score 64; DB 1; Length 71;
 Best Local Similarity 28.6%; Pred. No. 2;
 Matches 18; Conservative 7; Mismatches 16; Indels 22; Gaps 3;
 Query 25 LDGQDPADPRAEQMDDISSEHFLFKRQNCN-----GGCS-----63
 | | | | | : | | | | | : | | | | | : | | | | | :
 DB 4 LSEDDPAAQALE-YRHDASSVQHAYEGGQTCNLLYTDASQDNGPCSVFFGKLYSAN 62

QY 64 KWC 66
 DB 63 GWC 65
 RESULT 11
 YPJP_BACSU
 ID YPJP_BACSU STANDARD; PRT; 203 AA.
 AC P54172;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein YPJP.
 GN YPJP.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 [1]
 SEQUENCE FROM N.A.
 RP STRAIN=168 / Marburg;
 RC MEDLINE=96349105; PubMed=8760912;
 RA Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
 Sorokin P.;
 "Sequence analysis of the Bacillus subtilis chromosome region between
 the serA and kds loci cloned in a yeast artificial chromosome.";
 Microbiology 142:2005-2016(1996).
 [2]
 SEQUENCE FROM N.A.
 RP STRAIN=168;
 RC MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 Azevedo V., Bertsch M.G., Bessieres P., Bolotin A., Borchert S.,
 Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Henaut A.,
 Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Itaya M., Jones L.,
 Hilbert H., Holsappel S., Hosono S., Hullio M.F., Itaya M., Jones L.,
 Joris B., Karamata D., Kasahara Y., Klaere-Blanchard M., Klein C.,
 Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 Kurita K., Lapiou A., Lardinois S., Lauber J., Lazarevic V.,
 Lee S.M., Levine A., Liu H., Masuda S., Mael C., Medigue C.,
 Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis.";
 Nature 390:249-256(1997).
 [3]
 SEQUENCE OF 152-203 FROM N.A.
 RP STRAIN=168;
 RC MEDLINE=88284366; PubMed=2840350;
 RA Iwakura M., Kawata M., Tsuda K., Tanaka T.;
 "Nucleotide sequence of the thymidylate synthase B and dihydrofolate
 reductase genes contained in one Bacillus subtilis operon.";
 Gene 64:9-20(1988).
 CC -----
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -

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OM protein - protein search, using sw model

Run on: January 10, 2003, 08:32:32 ; Search time 45 Seconds
(without alignments)
343.412 Million cell updates/sec

Title: US-09-910-009A-210
Perfect score: 420
Sequence: 1 GMSKGLVLLTVCLLFLPL.....CNGGCGSKWCRDHARCCGR 75

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp-archaea.*
2: sp-bacteria.*
3: sp-fungi.*
4: sp-human.*
5: sp-invertebrate.*
6: sp-mammal.*
7: sp-mhc.*
8: sp-organelle.*
9: sp-phage.*
10: sp-plant.*
11: sp-rodent.*
12: sp-virus.*
13: sp-vertebrate.*
14: sp-unclassified.*
15: sp-ivirius.*
16: sp-bacteriap.*
17: sp-archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	297.5	70.8	67	5	Q9BPJ2 conus ventr
2	263	62.6	72	5	Q9BPJ5 conus texti
3	251.5	59.9	68	5	Q9BPJ7 conus texti
4	251	59.8	68	5	Q9BPJ8 conus texti
5	248.5	59.2	67	5	Q9BPJ1 conus arena
6	242.5	57.7	71	5	Q9BPJ3 conus texti
7	236.5	56.3	68	5	Q9BPJ9 conus texti
8	234	55.7	70	5	Q9BPJ6 conus penna
9	222	52.9	90	5	Q9BPJ4 conus texti
10	221.5	52.7	70	5	Q9BPJ7 conus texti
11	217.5	51.8	68	5	Q9BPJ0 conus texti
12	213	50.7	67	5	Q9BPJ4 conus texti
13	208	49.5	67	5	Q9BPJ6 conus texti
14	205	48.8	67	5	Q9BPJ3 conus texti
15	199.5	47.5	68	5	Q9BPJ9 conus texti
16	193	46.0	67	5	Q9BPJ7 conus ventr

17	190	45.2	67	5	Q9BPJ0 conus tessu
18	190	45.2	67	5	Q9BPJ8 conus tessu
19	190	45.2	67	5	Q9BPJ5 conus tessu
20	128	30.5	44	5	Q9BP54 conus tessu
21	124.5	29.6	72	5	Q9BPJ2 conus texti
22	122.5	28.2	70	5	Q9BPJ4 conus tessu
23	118.5	28.2	70	5	Q9BH51 conus tessu
24	117.5	28.0	70	5	Q9BPJ5 conus tessu
25	115.5	27.5	72	5	Q9BPJ8 conus tessu
26	115	27.4	70	5	Q9BPJ9 conus tessu
27	114.5	27.3	70	5	Q9BPJ0 conus ventr
28	112.5	26.8	71	5	Q9BPJ7 conus texti
29	112	26.7	41	5	Q9BPJ5 conus texti
30	110.5	26.3	71	5	Q9BPJ8 conus penna
31	107.5	25.6	68	5	Q9BPJ1 conus penna
32	103.5	24.6	69	5	Q9BPJ7 conus ventr
33	100	23.8	67	5	Q9BPJ3 conus arena
34	77.5	18.5	79	5	Q9BPJ8 conus texti
35	72.5	17.3	77	5	Q9BPJ0 conus ventr
36	71	16.9	193	6	Q9BPJ8 conus ventr
37	70	16.7	213	16	Q9VJ14 mycobacteri
38	69.5	16.5	159	16	Q9I0C1 pseudomonas
39	65	15.5	186	12	O72735 cowpox viru
40	64.5	15.4	76	5	Q9BPJ6 conus texti
41	64	15.2	74	5	Q9BPJ0 conus ventr
42	64	15.2	466	10	Q9ST61 solanum tub
43	64	15.2	644	13	Q9O974 gallus gall
44	63.5	15.1	174	11	Q9DAU7 mus musculu
45	63.5	15.1	839	16	Q9A5C9 caulobacter

ALIGNMENTS

RESULT 1
Q9BPJ2
ID Q9BPJ2 PRELIMINARY; PRT; 67 AA.
AC Q9BPJ2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Conotoxin scaffold III/IV.
OS Conus ventricosus (Mediterranean cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=117992;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides."
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF214932; AAG60360.1; -
SQ SEQUENCE 67 AA; 7399 MW; 04A221446546BE29 CRC64;

Query Match 70.8%; Score 297.5; DB 5; Length 67;
Best Local Similarity 75.0%; Pred. No. 9.8e-29;
Matches 54; Conservative 5; Mismatches 8; Indels 5; Gaps 1;
Qy 3 MMSKGLVLLTVCLLFLPLALDGDQPADRPAERQDDISSDEHPLFDKRONCCGCS 62
Db 1 MMSKGLALLTICLLLPFLTALPLDGDQPADRPAERQDDISSDEHPLFDKROCCGCS 60
Qy 63 SKWCRDHARCCG 74
Db 61 NCW-----PCCG 67
RESULT 2
Q9BPJ5
ID Q9BPJ5 PRELIMINARY; PRT; 72 AA.
AC Q9BPJ5;

Fri Jan 10 09:33:19 2003

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DE 01-JUN-2001 (TREMBlrel. 17, Created)
OS 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
OC 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Conotoxin scaffold III/IV.
OS Conus textile (Cloth-of-gold cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6494;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21105969; PubMed=11158371;
RX Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF214928; AAG60356.1;
SQ SEQUENCE 72 AA; 7820 MW; EE6B0CB5BB43320 CRC64;

Query Match 62.6%; Score 263; DB 5; Length 72;
Best Local Similarity 66.2%; Pred. No. 1.6e-24;
Matches 53; Conservative 4; Mismatches 7; Indels 16; Gaps 3;

Oy 3 MMSKLGVLTTVCLLFPALTALPLDGDQPADPAERMDDISSDEHPLFDKRONCCNGGCS 56
Db 1 MMSKLGVLTTICLLFPALTALPLDGDQPADPAERMDDISSDEHPLFDKRONCCNGGCS 60

Oy 57 --CNGGSSKWCARDHARCCG 74
Db 61 VACNMGCEP-----CCG 72

RESULT 3
Q9BPJ7 PRELIMINARY; PRT; 68 AA.
AC Q9BPJ7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Conotoxin scaffold III/IV.
OS Conus textile (Cloth-of-gold cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6494;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21105969; PubMed=11158371;
RX Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF214926; AAG60354.1;
SQ SEQUENCE 68 AA; 7603 MW; 54CA322FFA7CB1B0 CRC64;

Query Match 59.9%; Score 251.5; DB 5; Length 68;
Best Local Similarity 66.2%; Pred. No. 3.8e-23;
Matches 47; Conservative 8; Mismatches 11; Indels 5; Gaps 2;

Oy 4 MMSKLGVLTTVCLLFPALTALPLDGDQPADPAERMDDISSDEHPLFDKRONCCNGGCS 63
Db 1 MMSKLGVLTTICLLFPALTALPLDGDQPADPAERMDDISSDEHPLFDKRONCCNGGCS 57

Oy 64 KWCARDHARCCG 73
Db 58 -FCRFGCTPCC 67

RESULT 4
Q9BPJ8 PRELIMINARY; PRT; 68 AA.
AC Q9BPJ8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
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DE Conotoxin scaffold III/IV.
OS Conus arenatus (Sand-dusted cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89451;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21105969; PubMed=11158371;
RX Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF214925; AAG60353.1;
SQ SEQUENCE 68 AA; 7638 MW; 5D3B27B506B56828 CRC64;

Query Match 59.8%; Score 251; DB 5; Length 68;
Best Local Similarity 75.0%; Pred. No. 4.4e-23;
Matches 45; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 3 MMSKLGVLTTVCLLFPALTALPLDGDQPADPAERMDDISSDEHPLFDKRONCCNGGCS 62
Db 1 MMSKLGVLTTICLLFPALTALPLDGDQPADPAERMDDISSDEHPLFDKRONCCNGGCS 60

RESULT 5
Q9BPJ1 PRELIMINARY; PRT; 67 AA.
AC Q9BPJ1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Conotoxin scaffold III/IV.
OS Conus textile (Cloth-of-gold cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6494;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21105969; PubMed=11158371;
RX Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF214933; AAG60361.1;
SQ SEQUENCE 67 AA; 7364 MW; EF18D7A9F4ECAE5 CRC64;

Query Match 59.2%; Score 248.5; DB 5; Length 67;
Best Local Similarity 68.1%; Pred. No. 8.7e-23;
Matches 49; Conservative 5; Mismatches 13; Indels 5; Gaps 2;

Oy 3 MMSKLGVLTTVCLLFPALTALPLDGDQPADPAERMDDISSDEHPLFDKRONCCNGGCS 62
Db 1 MMSKLGVLTTICLLFPALTALPLDGDQPADPAERMDDISSDEHPLFDKRONCCNGGCS 60

Oy 63 SKWCARDHARCCG 74
Db 61 S--CNP---CCG 67

RESULT 6
Q9BPJ3 PRELIMINARY; PRT; 71 AA.
AC Q9BPJ3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Conotoxin scaffold III/IV.
OS Conus textile (Cloth-of-gold cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6494;
RN [1]
RN SEQUENCE FROM N.A.
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RX MEDLINE=21105969; PubMed=11158371;
 RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
 RA Fainzilber M.;
 RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
 RL Mol. Biol. Evol. 18:120-131(2001).
 DR EMBL; AF214930; AAG60358.1; -;
 SQ SEQUENCE 71 AA; 7836 MW; 1A4ACC90B6551360 CRC64;

Query Match 57.7%; Score 242.5; DB 5; Length 71;
 Best Local Similarity 61.5%; Pred. No. 4.9e-22;
 Matches 48; Conservative 6; Mismatches 9; Indels 15; Gaps 2;

QY 3 MMSKLGVLTVCLLPFLPTALPLDQDPADPAERMQDDISSDEHPLFDKRNCCN----58
 Db 1 MMSKLGALLIICLLLPFLTAFLDQDADPAERLQDDISSKHHFMDVRCCHPSTC 60

QY 59 ---GCSSKWCORHARCC 73
 Db 61 HMRKGCs-----RCC 70

RESULT 7
 Q9BPJ9 PRELIMINARY; PRT; 68 AA.
 AC Q9BPJ9; 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Conotoxin scaffold III/IV.
 OS Conus tessulatus.
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=101317;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=21105969; PubMed=11158371;
 RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
 RA Fainzilber M.;
 RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
 RL Mol. Biol. Evol. 18:120-131(2001).
 DR EMBL; AF214924; AAG60352.1; -;
 DR InterPro: IP0001230; Prenyl_site.
 DR PROSITE: PS00294; PRENYLIATION; UNKNOWN_1.
 SQ SEQUENCE 68 AA; 7526 MW; C6C4B30552DDC946 CRC64;

Query Match 56.3%; Score 236.5; DB 5; Length 68;
 Best Local Similarity 75.0%; Pred. No. 2.5e-21;
 Matches 45; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

QY 3 MMSKLGVLTVCLLPFLPTALPLDQDPADPAERMQDDISSDEHPLFDKRNCCNGCS 62
 Db 1 MMSKLGVLITICLLLPFLTAFLDQDADPAERMQ-DISSEHPLFDPVKRCDDWPTC 59

RESULT 8
 Q9BH61 PRELIMINARY; PRT; 70 AA.
 AC Q9BH61; 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Conotoxin scaffold III/IV precursor.
 OS Conus pennaceus (feathered cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=37335;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=21105969; PubMed=11158371;
 RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
 RA Fainzilber M.;
 RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
 RL Mol. Biol. Evol. 18:120-131(2001).

DR EMBL; AF215094; AAG60515.1; -;
 DR EMBL; AF214931; AAG60359.1; -;
 SQ SEQUENCE 70 AA; 7770 MW; 8A90EEDF3F90B301 CRC64;

Query Match 55.7%; Score 234; DB 5; Length 70;
 Best Local Similarity 65.7%; Pred. No. 5.2e-21;
 Matches 46; Conservative 5; Mismatches 13; Indels 6; Gaps 1;

QY 3 MMSKLGVLTVCLLPFLPTALPLDQDPADPAERMQDDISSDEHPLFDKRNCCNG---59
 Db 1 MMSKLGVLIIICLLLPFLTAFLDQDADPAERMQDDISSHHHPLFDPVKRCCKYGT 60

QY 60 ---GCSSKWC 66
 Db 61 CWLGCSPGCC 70

RESULT 9
 Q9BPJ4 PRELIMINARY; PRT; 90 AA.
 AC Q9BPJ4; 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Conotoxin scaffold III/IV.
 OS Conus textile (cloth-of-gold cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6494;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=21105969; PubMed=11158371;
 RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
 RA Fainzilber M.;
 RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
 RL Mol. Biol. Evol. 18:120-131(2001).
 DR EMBL; AF214929; AAG60357.1; -;
 SQ SEQUENCE 90 AA; 10030 MW; 08EAF35A0CAAE36B CRC64;

Query Match 52.9%; Score 222; DB 5; Length 90;
 Best Local Similarity 50.5%; Pred. No. 1.9e-19;
 Matches 47; Conservative 8; Mismatches 14; Indels 24; Gaps 3;

QY 3 MMSKLGVLTVCLLPFLPTALPLDQDPADPAERMQDDISSDEHPLFD---KRQN---55
 Db 1 MMSKLGVLITICLLLPFLTAFLDQDADPAERLQDDISSHHHPLMNSIRREQNOFM 60

QY 56 -----CCNGCCKWCORHARCC 74
 Db 61 SFTSVKLRDSRGCCGPTACMACGRP---CCG 90

RESULT 10
 Q9BPJ6 PRELIMINARY; PRT; 70 AA.
 AC Q9BPJ6; 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Conotoxin scaffold III/IV.
 OS Conus textile (cloth-of-gold cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6494;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=21105969; PubMed=11158371;
 RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
 RA Fainzilber M.;
 RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
 RL Mol. Biol. Evol. 18:120-131(2001).
 DR EMBL; AF214927; AAG60355.1; -;
 SQ SEQUENCE 70 AA; 7848 MW; 92825D82F3BA9B68 CRC64;

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Query Match          52.7%; Score 221.5; DB 5; Length 70;
Best Local Similarity 60.3%; Pred. No. 1.7e-19;
Matches 44; Conservative 10; Mismatches 12; Indels 7; Gaps 3;

QY 3 MMSKLGVLTVCLLFFLTPALPDGDPADPRAERMQDDISSDHEPLFDKRNCCNGG-C 61
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||| : ||| :
Db 1 MMSKLGALLTICLLFSLTAVPLDGDQHDADPAGRLQDRIPTEHDHFLFDKRNCCDSEC 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||| :

QY 62 S-SKWC RDHARC 73
      | | | | |
Db 61 SYS CW-----PCC 68

RESULT 11
Q9BP K0
ID Q9BP K0 PRELIMINARY; PRT; 68 AA.
AC Q9BP K0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Conotoxin scaffold III/IV.
OS Conus tessulatus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101317;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RX Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF214923; AAG60351.1; -
DR InterPro: IPR001230; Prenyl_site.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN.1.
DR SEQUENCE 68 AA; 7613 MW; E01C4202318BF9F9 CRC64;

Query Match          51.8%; Score 217.5; DB 5; Length 68;
Best Local Similarity 68.3%; Pred. No. 5.1e-19;
Matches 41; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 3 MMSKLGVLTVCLLFFLTPALPDGDPADPRAERMQDDISSDHEPLFDKRNCCNGGCS 62
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Db 1 MMSKLGVLTVCLLFFLTPALPDGDPADPRAERMQDDISSDHEPLFDKRNCCDMPCT 59
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RESULT 12
Q9BP I4
ID Q9BP I4 PRELIMINARY; PRT; 67 AA.
AC Q9BP I4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Conotoxin scaffold III/IV.
OS Conus tessulatus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101317;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RX Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF214940; AAG60368.1; -
DR SEQUENCE 67 AA; 7593 MW; 1A65FED58E8DD811 CRC64;

Query Match          50.7%; Score 213; DB 5; Length 67;
Best Local Similarity 60.6%; Pred. No. 1.8e-18;
Matches 43; Conservative 8; Mismatches 14; Indels 6; Gaps 3;

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Qy 63 SKWCRDHARCC 73
I::I II
Db 55 SRYCICIPC 65

RESULT 15

Q9BPI9 PRELIMINARY; PRT; 68 AA.
AC Q9BPI9;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Conotoxin scaffold III/IV.
OS Conus ventricosus (Mediterranean cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=117992;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF214935; AAG60363.1; -
SQ SEQUENCE 68 AA; 7536 MW; 487D0D94FAA393A CRC64;

Query Match 47.5%; Score 199.5; DB 5; Length 68;
Best Local Similarity 65.0%; Pred. No. 7.8e-17;
Matches 39; Conservative 6; Mismatches 14; Indels 1; Gaps 1;

Qy 3 MMSKLGVLTVCLLFLPLTALPLDGPADRPAPERMDDISSDEHPLFDKRONCCGGCS 62
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Db 1 MMSKLGVLITICLLFLPLTAVPMGDPADLPALRTQ-DFEPERSPWDFVRRCCSQDCS 59

Search completed: January 10, 2003, 08:37:35
Job time : 46 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 10, 2003, 08:32:32 ; Search time 22.1739 Seconds
(without alignments)
99.519 Million cell updates/sec

Title: US-09-910-009a-210

Perfect score: 420

Sequence: 1 GSMMSKLGVLVTFVLLLFPL.....CCNGCGSKWCARDHRCGR 75

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	223.5	53.2	68	1	US-07-689-693B-11
2	191.5	45.5	52	1	US-07-689-693B-24
3	73	17.4	333	2	US-08-700-442A-9
4	73	17.4	333	4	US-08-831-028-9
5	72.5	17.3	64	1	US-08-137-800-37
6	72.5	17.3	64	1	US-08-137-800-39
7	72.5	17.3	64	1	US-08-477-383-37
8	72.5	17.3	64	1	US-08-477-383-39
9	72.5	17.3	64	1	US-08-487-174-37
10	72.5	17.3	64	1	US-08-487-174-39
11	72.5	17.3	64	1	US-08-480-750-37
12	72.5	17.3	64	1	US-08-480-750-39
13	72.5	17.3	3025	6	5223423-3
14	71.5	17.0	59	4	US-09-488-799-31
15	71.5	17.0	63	3	US-09-061-026-22
16	71.5	17.0	63	4	US-09-466-138-22
17	70.5	16.8	63	3	US-09-061-026-14
18	70.5	16.8	63	4	US-09-466-138-14
19	70	16.7	27	1	US-08-599-556-7
20	68.5	16.3	63	3	US-09-061-026-16
21	68.5	16.3	63	4	US-09-466-138-16
22	65.5	15.6	59	4	US-09-488-799-33
23	65.5	15.6	59	4	US-09-488-799-37
24	65.5	15.6	64	1	US-07-689-693B-13
25	65.5	15.6	206	1	US-08-178-708-3
26	65.5	15.6	206	1	US-08-457-552-3
27	65.5	15.6	206	1	US-08-456-430-3

28	65.5	15.6	206	2	US-08-994-418-3	Sequence 3, Appli
29	65.5	15.6	206	5	PCT-US95-00432-3	Sequence 3, Appli
30	65	15.5	27	5	PCT-US96-05262-12	Sequence 12, Appl
31	63.5	15.1	64	1	US-08-137-800-36	Sequence 36, Appl
32	63.5	15.1	64	1	US-08-137-800-45	Sequence 36, Appl
33	63.5	15.1	64	1	US-08-477-383-36	Sequence 36, Appl
34	63.5	15.1	64	1	US-08-477-383-45	Sequence 36, Appl
35	63.5	15.1	64	1	US-08-487-174-36	Sequence 36, Appl
36	63.5	15.1	64	1	US-08-487-174-45	Sequence 36, Appl
37	63.5	15.1	64	1	US-08-480-750-36	Sequence 36, Appl
38	63.5	15.1	64	1	US-08-480-750-45	Sequence 36, Appl
39	63.5	15.1	174	4	US-09-724-864-56	Sequence 56, Appl
40	63	15.0	60	4	US-09-488-799-49	Sequence 49, Appl
41	63	15.0	60	4	US-09-488-799-51	Sequence 51, Appl
42	63	15.0	1417	4	US-08-900-230-3	Sequence 3, Appli
43	62.5	14.9	59	4	US-09-488-799-29	Sequence 29, Appl
44	62.5	14.9	59	4	US-09-488-799-75	Sequence 75, Appl
45	62.5	14.9	63	3	US-09-061-026-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-07-689-693B-11
; Sequence 11, Application US/07689693B
; Patent No. 5231011
; GENERAL INFORMATION:
; APPLICANT: David Hillyard
; APPLICANT: Baldomero M. Olivera
; TITLE OF INVENTION: Segregated Folding Determinants
; TITLE OF INVENTION: for Small Disulfide-Rich Peptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Thorpe, No. 5231011th & Western
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
; COMPUTER: Compaq LTE/286
; OPERATING SYSTEM: DOS 4.01
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/689,693B
; FILING DATE: 19910418
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: na
; ATTORNEY/AGENT INFORMATION:
; NAME: Western, M. Wayne
; REGISTRATION NUMBER: 22,788
; REFERENCE/DOCKET NUMBER: 9925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801) 566-6633
; TELEFAX: (801) 566-0750
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Prepropeptide sequence for three loop
; NAME/KEY: conotoxin from Circler conotoxin from Conus
; NAME/KEY: textile
; IDENTIFICATION METHOD: Libraries were created
; IDENTIFICATION METHOD: using oligo-dr primed pUC13 vector
US-07-689-693B-11

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Query Match          53.2%; Score 223.5; DB 1; Length 68;
Best Local Similarity 56.6%; Pred. No. 6.8e-18;
Matches          43; Conservative          9; Mismatches 11; Indels 13; Gaps 2;

QY      4  MSKLGVLLTVCLLLPPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRONC-----CN 58
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DB      1  MSKLGALLTICLLLSLTAVPLDGDQHADQPAORLQDRIPTEDHPLFDPNKRCCPPVACN 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      59  GGCSSKWCRRDHARCCG 74
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DB      61  MGCKP-----CCG 68

RESULT 2
US-07-689-693B-24
; Sequence 24, Application US/07689693B
; Patent No. 5231011
; GENERAL INFORMATION:
; APPLICANT: David Hillyard
; APPLICANT: Baldomero M. Olivera
; TITLE OF INVENTION: Segregated Folding Determinants
; TITLE OF INVENTION: for Small Disulfide-Rich Peptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, No. 5231011th & Western
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
; COMPUTER: Compaq LTE/286
; OPERATING SYSTEM: DOS 4.01
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/689,693B
; FILING DATE: 19910418
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: na
; ATTORNEY/AGENT INFORMATION:
; NAME: Western, M. Wayne
; REGISTRATION NUMBER: 22,788
; REFERENCE/DOCKET NUMBER: 9925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801) 566-6633
; TELEFAX: (801) 566-0750
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Signal/Pro sequence for synthesis of
; NAME/KEY: three loop conotoxin from Circler conotoxin
; IDENTIFICATION METHOD: Libraries were created
; IDENTIFICATION METHOD: using oligo-dt primed pUC13 vector
US-07-689-693B-24
      45.5%; Score 191; DB 1; Length 52;
Query Match
Best Local Similarity 72.9%; Pred. No. 1.9e-14;
Matches          35; Conservative          8; Mismatches 5; Indels 0; Gaps 0;

QY      4  MSKLGVLLTVCLLLPPLTALPLDGDQPADRPAERMQDDISSDEHPLFD 51
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      1  MSKLGALLTICLLLSLTAVPLDGDQHADQPAORLQDRIPTEDHPLFD 48

RESULT 3
US-08-700-442A-9

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ADDRESSEE: Zeneca, Inc.
STREET: 1200 South 47th Street
CITY: Richmond
STATE: CA
COUNTRY: USA
ZIP: 94804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,028
FILING DATE: 04-APR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/700,442
FILING DATE: 19-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00509
FILING DATE: 09-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9404807.1
FILING DATE: 11-MAR-1994
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: FIGURE 10
US-08-831-028-9

Query Match 17.4%; Score 73; DB 4; Length 333;
Best Local Similarity 28.0%; Pred. No. 1.2;
Matches 23; Conservative 13; Mismatches 26; Indels 20; Gaps 4;
QY 4 MSKLGVLTVCLLLFPLTAL-----PLDGDQPADRPAPAE-----RMQDDISSDEHPLEFD 51
DB 1 MVQGVVFGVLLILFICSTLSADSKPNPTKEEPAPKPDVSVKSGPEVSEDQY----- 56
QY 52 KRQNCNGCGSSKWCRRHARCC 73
DB 57 -RHRCACWGPGRKYCK---RWC 74

RESULT 5
US-08-137-800-37
Sequence 37, Application US/08137800
Patent No. 5514774
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Santos, Ameurina D.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800

FILING DATE: 19-OCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-104763
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Conus striatus
US-08-137-800-37
Query Match 17.3%; Score 72.5; DB 1; Length 64;
Best Local Similarity 31.4%; Pred. No. 0.25;
Matches 22; Conservative 11; Mismatches 24; Indels 13; Gaps 4;
QY 9 VLLTVCLLLFPLTALPLDGDQPADRPAPAE---DISSEHPLEFKRQNCNGCGSSKW 65
DB 5 MMFTVELLVLATTVV---SFFSDRASDGRDDEAKDERSDMHE-SDRKEICCNACGPKY 60
QY 66 CRDHARCCGR 75
DB 61 -----SCGR 64

RESULT 6
US-08-137-800-39
Sequence 39, Application US/08137800
Patent No. 5514774
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Santos, Ameurina D.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-OCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-104763
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
TOPOLOGY: linear

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; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus striatus
US-08-137-800-39

Query Match 17.3%; Score 72.5; DB 1; Length 64;
Best Local Similarity 31.4%; Pred. No. 0.25;
Matches 22; Conservative 11; Mismatches 24; Indels 13; Gaps 4;

QY 9 VLLTVCLLLFLPLTALPDGDPADRPARMQD--DISSDHPLFDKRONCCNGCGSSKW 65
Db 5 MMFTVFLVLVIATTV---SFPDSRASDGRDDEAKDERSDMHE-SDRKEICCNPCAGPKY 60
QY 66 CRDHARCCGR 75
Db 61 -----SCGR 64

RESULT 7
US-08-477-383-37
; Sequence 37, Application US/08477383
; Patent No. 5589340
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurfino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,383
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,848
; FILING DATE: 29-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107673
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus striatus
US-08-477-383-37

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QY 66 CRDHARCCGR 75
 Db 61 -----SCGR 64

RESULT 9
 US-08-487-174-37
 ; Sequence 37, Application US/08487174
 ; Patent No. 5595972
 ; GENERAL INFORMATION:
 ; APPLICANT: Olivera, Baldomero M.
 ; APPLICANT: Cruz, Lourdes J.
 ; APPLICANT: Hillyard, David R.
 ; APPLICANT: Macintosh, J. Michael
 ; APPLICANT: Santos, Aneurfino S.
 ; TITLE OF INVENTION: Conotoxin Peptides
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 ; STREET: 1201 New York Avenue, N.W., Suite 1000
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,174
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/137,800
 ; FILING DATE: 19-OCT-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/084,848
 ; FILING DATE: 29-JUN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ihnen, Jeffrey L.
 ; REGISTRATION NUMBER: 28,957
 ; REFERENCE/DOCKET NUMBER: 24260-107673
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-962-8300
 ; TELEFAX: 202-962-8300
 ; INFORMATION FOR SEQ ID NO: 37:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 64 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Conus striatus
 ; US-08-487-174-37

Query Match 17.3%; Score 72.5; DB 1; Length 64;
 Best Local Similarity 31.4%; Pred. No. 0.25;
 Matches 22; Conservative 11; Mismatches 24; Indels 13; Gaps 4;
 QY 9 VLLTVCLLLPPLTALPLDGPADPRPAERMQD---DISSDEHPLFDKRNCCNGCGSSKW 65
 Db 5 MMFTVFLVLLVLTATTVV---SFPSDRASDRGRDEAKDRSDMHE-SDRKEICCNPCACGPKY 60
 QY 66 CRDHARCCGR 75
 Db 61 -----SCGR 64

RESULT 10

US-08-487-174-39
 ; Sequence 39, Application US/08487174
 ; Patent No. 5595972
 ; GENERAL INFORMATION:
 ; APPLICANT: Olivera, Baldomero M.
 ; APPLICANT: Cruz, Lourdes J.
 ; APPLICANT: Hillyard, David R.
 ; APPLICANT: Macintosh, J. Michael
 ; APPLICANT: Santos, Aneurfino S.
 ; TITLE OF INVENTION: Conotoxin Peptides
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 ; STREET: 1201 New York Avenue, N.W., Suite 1000
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,174
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/137,800
 ; FILING DATE: 19-OCT-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/084,848
 ; FILING DATE: 29-JUN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ihnen, Jeffrey L.
 ; REGISTRATION NUMBER: 28,957
 ; REFERENCE/DOCKET NUMBER: 24260-107673
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-962-4810
 ; TELEFAX: 202-962-8300
 ; INFORMATION FOR SEQ ID NO: 39:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 64 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Conus striatus
 ; US-08-487-174-39

Query Match 17.3%; Score 72.5; DB 1; Length 64;
 Best Local Similarity 31.4%; Pred. No. 0.25;
 Matches 22; Conservative 11; Mismatches 24; Indels 13; Gaps 4;
 QY 9 VLLTVCLLLPPLTALPLDGPADPRPAERMQD---DISSDEHPLFDKRNCCNGCGSSKW 65
 Db 5 MMFTVFLVLLVLTATTVV---SFPSDRASDRGRDEAKDRSDMHE-SDRKEICCNPCACGPKY 60
 QY 66 CRDHARCCGR 75
 Db 61 -----SCGR 64

RESULT 11
 US-08-480-750-37
 ; Sequence 37, Application US/08480750
 ; Patent No. 5633347
 ; GENERAL INFORMATION:
 ; APPLICANT: Olivera, Baldomero M.
 ; APPLICANT: Cruz, Lourdes J.
 ; APPLICANT: Hillyard, David R.

us-09-910-009a-210.rai

Fri Jan 10 09:33:17 2003

APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Aneurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,750
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus striatus
US-08-480-750-37

Query Match 17.3%; Score 72.5; DB 1; Length 64;
Best Local Similarity 31.4%; Pred. No. 0.25;
Matches 22; Conservative 11; Mismatches 24; Indels 13; Gaps 4;

QY 9 VLLTVCLLLFPLTALPLDGDQPADRAERMQD---DISSDHPLFDKRONCCNGCGSSKW 65
Db 5 MMFTVLLVVLATTVV---SFPSDRASDGRDDEAKDERSDMHE-SDRKEICCNPCAGPKY 60
QY 66 CRDHARCCGR 75
Db 61 -----SCGR 64

RESULT 12
US-08-480-750-39
Sequence 39, Application US/08480750
Patent No. 5633347
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Aneurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000

CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,750
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus striatus
US-08-480-750-39

Query Match 17.3%; Score 72.5; DB 1; Length 64;
Best Local Similarity 31.4%; Pred. No. 0.25;
Matches 22; Conservative 11; Mismatches 24; Indels 13; Gaps 4;

QY 9 VLLTVCLLLFPLTALPLDGDQPADRAERMQD---DISSDHPLFDKRONCCNGCGSSKW 65
Db 5 MMFTVLLVVLATTVV---SFPSDRASDGRDDEAKDERSDMHE-SDRKEICCNPCAGPKY 60
QY 66 CRDHARCCGR 75
Db 61 -----SCGR 64

RESULT 13
5223423-3
Patent No. 5223423
APPLICANT: FRANCHINI, GENOVEFFA, WONG-STAAAL, FLOSSIE;
GALLO, ROBERT
TITLE OF INVENTION: CHARACTERIZATION OF REPLICATION COMPETENT
HUMAN IMMUNODEFICIENCY TYPE 2 PROVIRAL CLONE HIV-2 SBL/ISY
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/331,212
FILING DATE: 03-31-1989
SEQ ID NO: 3
LENGTH: 3025
5223423-3

Query Match 17.3%; Score 72.5; DB 6; Length 3025;
Best Local Similarity 23.7%; Pred. No. 13;
Matches 22; Conservative 14; Mismatches 24; Indels 33; Gaps 4;

QY 6 KLGVLTVCLLLFPLTALPLDQ-----DQPADRAERMQDDISSDE----- 46
Db 1821 KLSILTLACLLLATITSLDMEPLKAPESSLGSYNPSRTSEQ---DVAOTELANOGEE 1877

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OM protein - protein search, using sw model

Run on: January 10, 2003, 08:32:27 ; Search time 26.2609 Seconds
(without alignments)
101.482 Million cell updates/sec

Title: US-09-910-009a-211

Perfect score: 121

Sequence: 1 XNCCNGGCSKXCRDHACC 20

Scoring table: BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	118	97.5	20	23	AB88284
2	117	96.7	20	23	AB88449
3	117	96.7	75	23	AB88283
4	95	78.5	22	23	AB88345
5	94	77.7	22	23	AB88490
6	94	77.7	76	23	AB88344
7	73	60.3	22	23	AB88395
8	72	59.5	22	23	AB88491
9	72	59.5	74	23	AB88394
10	71	58.7	26	23	AB88168

11	70.5	58.3	23	23	AB88164	C bullatus mu-cono
12	70	57.9	26	23	AB88512	C bullatus mu-cono
13	70	57.9	80	23	AB88167	C bullatus mu-cono
14	69.5	57.4	23	23	AB88510	C bullatus mu-cono
15	69.5	57.4	77	23	AB88163	C bullatus mu-cono
16	66	54.5	24	23	AB88166	C bullatus mu-cono
17	65	53.7	24	23	AB88511	C bullatus mu-cono
18	65	53.7	78	23	AB88165	C bullatus mu-cono
19	63.5	52.5	23	23	AB88162	C bullatus mu-cono
20	61.5	50.8	23	23	AB88509	C bullatus mu-cono
21	61.5	50.8	77	23	AB88161	C bullatus mu-cono
22	58	47.9	134	22	AB844596	Human wound healin
23	58	47.9	175	22	AB844606	Human wound healin
24	58	47.9	224	22	ABG20306	Novel human diagno
25	57.5	47.5	21	23	AB88300	C tulipa mu-conope
26	57.5	47.5	21	23	AB88533	C tulipa mu-conope
27	57.5	47.5	21	23	AB88534	C tulipa mu-conope
28	57.5	47.5	74	23	AB88299	C tulipa mu-conope
29	57.5	47.5	75	23	AB88318	C tulipa mu-conope
30	57	47.1	1679	22	AAU07343	1-aminocyclopropan
31	56.5	46.7	21	23	AB88319	C tulipa mu-conope
32	54	44.6	3680	22	AB870878	Drosophila melanog
33	53	43.8	167	22	AA39466	Human polypeptide
34	53	43.8	222	22	AA41252	Human polypeptide
35	53	43.8	229	22	AA79404	Human protein SEQ
36	53	43.8	1329	23	AAU91279	Human NOV3a protei
37	52	43.0	86	22	AAU54875	Propionibacterium
38	51	42.1	23	23	AB88150	C auriacus mu-co
39	51	42.1	23	23	AB88262	C nobilis mu-conop
40	51	42.1	23	23	AB88278	C stercusmuscarum
41	51	42.1	23	23	AB88321	C auriacus mu-co
42	51	42.1	23	23	AB88507	C auriacus mu-co
43	51	42.1	23	23	AB88508	C auriacus mu-co
44	51	42.1	23	23	AB88526	C nobilis mu-conop
45	51	42.1	23	23	AB88532	C stercusmuscarum

ALIGNMENTS

RESULT 1
AB88284
ID AB88284 standard; Peptide: 20 AA.
XX AC AB88284;
XX DT 24-MAY-2002 (first entry)
XX DE C striatus mu-conopeptide S3-2.
XX KW Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
XX KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
XX KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
XX KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
XX KW neurodegenerative disease; neuromuscular disorder.
XX OS Conus striatus.
XX FH Key Location/Qualifiers
XX FT Misc-difference 1 /label= Gln, OTHER
XX FT FT /note= "OTHER-pyroGlu"
XX FT Misc-difference 12 /label= Trp, OTHER
XX FT FT /note= "bromo-Trp"
XX WO200207678-A2.
XX PD 31-JAN-2002.
XX XX 23-JUL-2001; 2001WO-US23125.
XX XX 21-JUL-2000; 2000US-219619P.

PI Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX WPI; 2002-217020/27.
 XX New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 XX Claim 1; Page 83; 231pp; English.
 XX The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide of the invention.
 XX SQ Sequence 22 AA;
 Query Match 77.7%; Score 94; DB 23; Length 22;
 Best Local Similarity 75.0%; Pred. No. 0.00033;
 Matches 15; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
 QY 3 CCNG--GCSSKXCRDHARCC 20
 |||| ||||: ||||: ||||
 Db 3 CCNGRGCSSRWCRDHSRCC 22
 RESULT 6
 ABB88344
 ID ABB88344 standard; Protein; 76 AA.
 XX AC ABB88344;
 XX 24-MAY-2002 (first entry)
 XX C stercusmuscarum mu-conopeptide Sm3-3 propeptide.
 DE Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 DE anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.
 XX Conus stercusmuscarum.
 OS
 XX Key Location/Qualifiers
 FT Misc-difference 7 /label= Pro, OTHER
 FT /note= "OTHER-hydroxy-Pro"
 FT Misc-difference 14 /label= Trp, OTHER
 FT /note= "OTHER-Bromo-Trp"
 XX WO200207678-A2.
 XX 31-JAN-2002.
 XX 23-JUL-2001; 2001WO-US23125.
 XX 21-JUL-2000; 2000US-219619P.
 PR 03-NOV-2000; 2000US-245157P.
 PR 29-JAN-2001; 2001US-264319P.
 PR 21-MAR-2001; 2001US-277270P.
 XX (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX WPI; 2002-217020/27.

DR N-PSDB; ABL88578.
 XX New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 XX Claim 9; Page 69; 231pp; English.
 XX The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide preprotein of the invention.
 XX SQ Sequence 76 AA;
 Query Match 77.7%; Score 94; DB 23; Length 76;
 Best Local Similarity 75.0%; Pred. No. 0.00089;
 Matches 15; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
 QY 3 CCNG--GCSSKXCRDHARCC 20
 |||| ||||: ||||: ||||
 Db 54 CCNGRGCSSRWCRDHSRCC 73
 RESULT 7
 ABB88395
 ID ABB88395 standard; Peptide; 22 AA.
 XX AC ABB88395;
 XX 24-MAY-2002 (first entry)
 XX C consors mu-conopeptide Cn3-3.
 XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.
 XX Conus consors.
 OS
 XX Key Location/Qualifiers
 FT Misc-difference 7 /label= Pro, OTHER
 FT /note= "OTHER-hydroxy-Pro"
 FT Misc-difference 14 /label= Trp, OTHER
 FT /note= "OTHER-Bromo-Trp"
 XX WO200207678-A2.
 XX 31-JAN-2002.
 XX 23-JUL-2001; 2001WO-US23125.
 XX 21-JUL-2000; 2000US-219619P.
 PR 03-NOV-2000; 2000US-245157P.
 PR 29-JAN-2001; 2001US-264319P.
 PR 21-MAR-2001; 2001US-277270P.
 XX (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.

XX PI Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 XX PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX DR WPI: 2002-217020/27.
 XX PT New mu-conopeptides useful for treating disorders associated with
 XX PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 XX PT blocking agents, as local anesthetic agents, as analgesic agents and as
 XX PT neuroprotective agents -
 XX PS Claim 1; Page 80; 231pp; English.
 XX CC The present invention relates to mu-conopeptides derived from snails,
 XX CC which can be in the treatment of disorders associated with voltage-gated
 XX CC ion channels. These may include neurodegenerative disorders such as
 XX CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 XX CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 XX CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 XX CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 XX CC or ischaemia which typically follows stroke, cerebrovascular accident,
 XX CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 XX CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 XX CC providing muscle relaxation, treating essential blepharospasm and other
 XX CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 XX CC is a mu-conopeptide of the invention.
 XX SQ Sequence 22 AA;

Query Match 60.3%; Score 73; DB 23; Length 22;
 Best Local Similarity 60.0%; Pred. No. 0.071;
 Matches 12; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 3 CCN--GGCSSKXCRDHARCC 20
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 DB 3 CCDVXNACSGRXCRDHAQCC 22

RESULT 8

ABB88491
 ID ABB88491 standard; Peptide; 22 AA.

XX AC ABB88491;

XX DT 24-MAY-2002 (first entry)

XX DE C consors mu-conopeptide SEQ ID NO: 474.

XX KW Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.

XX OS Conus consors.

XX PN WO200207678-A2.

XX PD 31-JAN-2002.

XX PF 23-JUL-2001; 2001WO-US23125.

XX PR 21-JUL-2000; 2000US-219619P.

XX PR 03-NOV-2000; 2000US-245157P.

XX PR 29-JAN-2001; 2001US-264319P.

XX PR 21-MAR-2001; 2001US-277270P.

XX PA (UTAH) UNIV UTAH RES FOUND.

XX PA (COGN-) COGNETIX INC.

XX PI Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;

XX PI Jacobsen R, Jones RM, Cartier GE, Shen GS;

XX PT

DR WPI: 2002-217020/27.

XX PT New mu-conopeptides useful for treating disorders associated with
 XX PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 XX PT blocking agents, as local anesthetic agents, as analgesic agents and as
 XX PT neuroprotective agents -

XX PS Claim 1; Page 83; 231pp; English.

XX CC The present invention relates to mu-conopeptides derived from snails,
 XX CC which can be in the treatment of disorders associated with voltage-gated
 XX CC ion channels. These may include neurodegenerative disorders such as
 XX CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 XX CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 XX CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 XX CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 XX CC or ischaemia which typically follows stroke, cerebrovascular accident,
 XX CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 XX CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 XX CC providing muscle relaxation, treating essential blepharospasm and other
 XX CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 XX CC is a mu-conopeptide of the invention.

XX SQ Sequence 22 AA;

Query Match 59.5%; Score 72; DB 23; Length 22;

Best Local Similarity 55.0%; Pred. No. 0.092;

Matches 11; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 3 CCN--GGCSSKXCRDHARCC 20

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 DB 3 CCDVXNACSGRXCRDHAQCC 22

RESULT 9

ABB88394

ID ABB88394 standard; Protein; 74 AA.

XX AC ABB88394;

XX DT 24-MAY-2002 (first entry)

XX DE C consors mu-conopeptide Cn3-3 propeptide.

XX KW Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.

XX OS Conus consors.

XX PN WO200207678-A2.

XX PD 31-JAN-2002.

XX PF 23-JUL-2001; 2001WO-US23125.

XX PR 21-JUL-2000; 2000US-219619P.

XX PR 03-NOV-2000; 2000US-245157P.

XX PR 29-JAN-2001; 2001US-264319P.

XX PR 21-MAR-2001; 2001US-277270P.

XX PA (UTAH) UNIV UTAH RES FOUND.

XX PA (COGN-) COGNETIX INC.

XX PI Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;

XX PI Jacobsen R, Jones RM, Cartier GE, Shen GS;

XX DR WPI: 2002-217020/27.

XX DR N-PSDB; ABL88603.

XX PT New mu-conopeptides useful for treating disorders associated with

New mu-conopeptides useful for treating disorders associated with voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular blocking agents, as local anesthetic agents, as analgesic agents and as neuroprotective agents	-
PPT	
XX	
PS	Claim 1; Page 29; 231pp; English.
XX	
CC	The present invention relates to mu-conopeptides derived from snails, which can be in the treatment of disorders associated with voltage-gated ion channels. These may include neurodegenerative disorders such as amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuronal pain and phantom limb, burn pain, epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, providing muscle relaxation, treating essential blepharospasm and other forms of focal dystonia, and for anti-wrinkle use. The present sequence is a mu-conopeptide of the invention.
CC	
XX	
SO	Sequence 26 AA;

	Query Match	58.7%	Score 71;	DB 23;	Length 26;
	Best Local Similarity	60.9%;	Pred. NO.	0.14;	
	Matches 14;	Conservative	2;	Mismatches	1; Indels
	Gaps	6;	Gaps	2;	
QY	3 CCN-----GGCSSKXCRDHAPCC	20			
		:			
db	5 CCNKGNKRKC-SRXCRDHSRCC	26			

RESULT 11
ABB88164
ID ABB88164 standard; Peptide; 23 AA.

XX	
AC	ABB88164;
XX	
DT	24-MAY-2002 (first entry)
XX	
DE	C bullatus mu-conopeptide Bu3-1A.
XX	
KW	Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
KW	anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
KW	cerebroprotective; anticonvulsant; antitumor; antidiabetic;
KW	cardiovascular; vasotropic; cardiac; tranquilizer; antimigraine;
KW	neurodegenerative disease; neuromuscular disorder.

XX	Cones	Qualifiers
XX	Key	Location/Qualifiers
FH	Misc-difference	15
FT		/label= Trp, OTHER
FT		/note= "OTHER=bromo-Trp"

XX
PN WO200207678-A2.

XX
PD 31-JAN-2002.

23-JUL-2001: 2001WO-US23125.

F1 ZS 00T 2001; 2001WC 0523123
 XX
 PR 21-JUL-2000; 2000US-219619P;

PR 21-OCT-2000; 2000US-245157P.
PR 03-NOV-2000; 2000US-245157P.
PR 29-JAN-2001; 2001US-264319P.

PR 29-JAN-2001; 2001US 204319P.
PR 21-MAR-2001; 2001US-277270P.
YY

XX (UTAH) UNIV UTAH RES FOUND.
PA (COGN-) COGNETIX INC
PA

PA
(COGN-) COGNELLA INC.
XX
PI Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
PI Jacobsen R, Jones RM, Cartier GE, Shen GS;

PI Oliveira BM, McInloosh CM, Gullerud GE, Wacklin
PI Jacobsen R, Jones BM, Cartier GE, Shen GS,

XX
DR WPI: 2002-217020/27.

10/20/07 11:11 AM

XX New mu-conopeptides useful for treating disorders associated with
PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
PT blocking agents, as local anesthetic agents, as analgesic agents and as
PT neuroprotective agents
XX
PS Claim 1; Page 29; 231pp; English.
XX
CC The present invention relates to mu-conopeptides derived from snails,
CC which can be in the treatment of disorders associated with voltage-gated
CC ion channels. These may include neurodegenerative disorders such as
CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
CC or ischaemia which typically follows stroke, cerebrovascular accident,
CC brain or spinal cord trauma, myocardial infarct, physical trauma,
CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
CC providing muscle relaxation, treating essential blepharospasm and other
CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
CC is a mu-conopeptide of the invention.
XX
SQ Sequence 23 AA;

Query Match 58.3%; Score 70.5; DB 23; Length 23;
Best Local Similarity 65.0%; Pred. No. 0.14;
Matches 13; Conservative 2; Mismatches 2; Indels 3; Gaps 2;

QY 3 CCNG--GCSSKXCRDHARCC 20
||| || : |||||:|
DB 5 CCKGKRGCC-GRXCRDHSRCC 23

RESULT 12
ABB88512
ID ABB88512 standard; Peptide; 26 AA.

XX ABB88512;
XX
XX 24-MAY-2002 (first entry)
XX
XX C bullatus mu-conopeptide SEQ ID NO: 495.
XX
XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
XX anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
XX cerebroprotective; anticonvulsant; antiaging; antidiabetic;
XX cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
XX neurodegenerative disease; neuromuscular disorder.

XX Conus bullatus.
XX
XX WO200207678-A2.
XX
XX 31-JAN-2002.
XX
XX 23-JUL-2001; 2001WO-US23125.
XX
XX 21-JUL-2000; 2000US-219619P.
XX 03-NOV-2000; 2000US-245157P.
XX 29-JAN-2001; 2001US-264319P.
XX 21-MAR-2001; 2001US-277270P.

XX (UTAH) UNIV UTAH RES FOUND.
XX (COGN-) COGNETIX INC.
XX
XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
XX Jacobsen R, Jones RM, Cartier GE, Shen GS;
XX
XX WPI; 2002-217020/27.

XX New mu-conopeptides useful for treating disorders associated with
PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
PT blocking agents, as local anesthetic agents, as analgesic agents and as

PT neuroprotective agents
XX
XX Claim 1; Page 84; 231pp; English.
XX
CC The present invention relates to mu-conopeptides derived from snails,
CC which can be in the treatment of disorders associated with voltage-gated
CC ion channels. These may include neurodegenerative disorders such as
CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
CC or ischaemia which typically follows stroke, cerebrovascular accident,
CC brain or spinal cord trauma, myocardial infarct, physical trauma,
CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
CC providing muscle relaxation, treating essential blepharospasm and other
CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
CC is a mu-conopeptide of the invention.
XX
SQ Sequence 26 AA;

Query Match 57.9%; Score 70; DB 23; Length 26;
Best Local Similarity 56.5%; Pred. No. 0.18;
Matches 13; Conservative 2; Mismatches 2; Indels 6; Gaps 2;

QY 3 CCN-----GCSSKXCRDHARCC 20
||| || : |||||:|
DB 5 CCNKGNGKRGCC-SRWCRDHSRCC 26

RESULT 13
ABB88167
ID ABB88167 standard; Protein; 80 AA.

XX ABB88167;
XX
XX 24-MAY-2002 (first entry)
XX
XX C bullatus mu-conopeptide Bu3-3 propeptide.

XX Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
XX anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
XX cerebroprotective; anticonvulsant; antiaging; antidiabetic;
XX cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
XX neurodegenerative disease; neuromuscular disorder.

XX Conus bullatus.
XX
XX WO200207678-A2.
XX
XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US23125.
XX
XX 21-JUL-2000; 2000US-219619P.
XX 03-NOV-2000; 2000US-245157P.
XX 29-JAN-2001; 2001US-264319P.
XX 21-MAR-2001; 2001US-277270P.

XX (UTAH) UNIV UTAH RES FOUND.
XX (COGN-) COGNETIX INC.
XX
XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
XX Jacobsen R, Jones RM, Cartier GE, Shen GS;
XX
XX WPI; 2002-217020/27.
XX N-PSDB; ABL88496.

XX New mu-conopeptides useful for treating disorders associated with
PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
PT blocking agents, as local anesthetic agents, as analgesic agents and as
PT neuroprotective agents
XX
XX Claim 9; Page 29; 231pp; English.

XX The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as
 CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide preprotein of the invention.

XX SQ Sequence 80 AA;

Query Match 57.9%; Score 70; DB 23; Length 80;
 Best Local Similarity 56.5%; Pred. No. 0.44;
 Matches 13; Conservative 2; Mismatches 2; Indels 6; Gaps 2;

QY 3 CCNKGKRGCC-SRWCRDHSRCC 20
 III III : III:III
 Db 56 CCNKGKRGCC-SRWCRDHSRCC 77

RESULT 14
 ABB88510
 ID ABB88510 standard; Peptide; 23 AA.
 XX AC ABB88510;
 XX DT 24-MAY-2002 (first entry)
 XX DE C bullatus mu-conopeptide SEQ ID NO: 493.
 XX KW Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.

XX OS Conus bullatus.
 XX PN WO200207678-A2.
 XX PD 31-JAN-2002.
 XX PF 23-JUL-2001; 2001WO-US23125.
 XX PR 21-JUL-2000; 2000US-219619P.
 PR 03-NOV-2000; 2000US-245157P.
 PR 29-JAN-2001; 2001US-264319P.
 PR 21-MAR-2001; 2001US-277270P.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX PI Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX DR WPI; 2002-217020/27.
 XX PT New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 XX PS Claim 1; Page 84; 23lpp; English.

XX The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as

CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
 CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide of the invention.

XX SQ Sequence 23 AA;

Query Match 57.4%; Score 69.5; DB 23; Length 23;
 Best Local Similarity 60.0%; Pred. No. 0.18;
 Matches 12; Conservative 2; Mismatches 3; Indels 3; Gaps 2;

QY 3 CCNG--GCSSKXCRDHARCC 20
 III II : III:III
 Db 5 CCKGRGCC-GRWCRDHSRCC 23

RESULT 15
 ABB88163
 ID ABB88163 standard; Protein; 77 AA.
 XX AC ABB88163;
 XX DT 24-MAY-2002 (first entry)
 XX DE C bullatus mu-conopeptide Bu3-1A propeptide.
 XX KW Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
 KW anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
 KW cerebroprotective; anticonvulsant; antiaging; antidiabetic;
 KW cardiovascular; vasotropic; cardiant; tranquilizer; antimigraine;
 KW neurodegenerative disease; neuromuscular disorder.

XX OS Conus bullatus.
 XX PN WO200207678-A2.
 XX PD 31-JAN-2002.
 XX PF 23-JUL-2001; 2001WO-US23125.
 XX PR 21-JUL-2000; 2000US-219619P.
 PR 03-NOV-2000; 2000US-245157P.
 PR 29-JAN-2001; 2001US-264319P.
 PR 21-MAR-2001; 2001US-277270P.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX PI Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE, Shen GS;
 XX DR WPI; 2002-217020/27.
 XX PT New mu-conopeptides useful for treating disorders associated with
 PT voltage-gated sodium channels, e.g. stroke or pain, as neuromuscular
 PT blocking agents, as local anesthetic agents, as analgesic agents and as
 PT neuroprotective agents -
 XX PS Claim 9; Page 28; 23lpp; English.

XX The present invention relates to mu-conopeptides derived from snails,
 CC which can be in the treatment of disorders associated with voltage-gated
 CC ion channels. These may include neurodegenerative disorders such as,
 CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
 CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
 CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,

CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
 CC or ischaemia which typically follows stroke, cerebrovascular accident,
 CC brain or spinal cord trauma, myocardial infarct, physical trauma,
 CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
 CC providing muscle relaxation, treating essential blepharospasm and other
 CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
 CC is a mu-conopeptide preprotein of the invention.

XX Sequence 77 AA;

Query Match 57.4%; Score 69.5; DB 23; Length 77;
 Best Local Similarity 60.0%; Pred. No. 0.48;
 Matches 12; Conservative 2; Mismatches 3; Indels 3; Gaps 2;

Qy 3 CCNG--GCSSKXCRDHARCC 20
 ||| || : |||||
 Db 56 CCKGKRGK-GWCRDHSRCC 74

Search completed: January 10, 2003, 08:35:35
 Job time : 27.5942 secs

Result No.	Score	Query %			DB	ID	Description
		Match	Length	DB			
1	53	43.8	223	2	B38346	ultra-high-sulfur	
2	53	43.8	230	2	A38346	ultra-high-sulfur	
3	52	43.0	169	1	S18946	ultra high-sulfur	
4	51.5	42.6	63	2	A34484	metallothionein I	
5	51	42.1	454	2	H86231	hypothetical prote	
6	50.5	41.7	147	2	T49670	conserved hypothet	
7	50	41.3	389	2	T46722	oryzanin (EC 3.4.22	
8	50	41.3	471	1	KRZ08	G protein-coupled	
9	49	40.5	1115	2	S40241	metallothionein 20	
10	48.5	40.1	71	2	S47576	metallothionein 20	
11	48.5	40.1	71	2	S39420	metallothionein 20	
12	48.5	40.1	71	2	S39421	metallothionein 20	
13	48.5	40.1	152	2	T18975	hypothetical prote	
14	48.5	40.1	164	2	T24272	hypothetical prote	
15	48.5	40.1	493	2	T01206	hypothetical prote	
16	48	39.7	263	2	A54648	cysteine proteinas	
17	48	39.7	1372	2	T25933	stannocalcin prec	
18	47	38.8	82	2	E36787	hypothetical prote	
19	47	38.8	87	2	S38929	hypothetical prote	
20	47	38.8	188	2	JC6547	pdxj protein - Aqu	
21	47	38.8	188	2	T15651	high sulfur protei	
22	47	38.8	164	2	T24602	hypothetical prote	
23	47	38.8	1297	2	T30274	cysteine proteinas	
24	46.5	38.4	72	2	S39416	proteoliasin - se	
25	46.5	38.4	72	2	S39419	metallothionein 10	
26	46.5	38.4	72	2	S39417	metallothionein 10	
27	46.5	38.4	593	1	GHU	granulin precursor	
28	46	38.0	29	2	A58537	omega-conotoxin MV	
29	46	38.0	63	2	A34905	metallothionein 1	

Fri Jan 10 09:33:20 2003

A:Residues: 1-63 <MEH>
A:Cross-references: GB:J05133; NID:g173321; PIDN:AAA35272.1; PID:g173322
A:Note: the authors translated the codon GAG for residue 61 as Asp
C:Superfamily: metallothionein

Query Match 42.6%; Score 51.5; DB 2; Length 63;
Best Local Similarity 50.0%; Pred. No. 8.7;
Matches 9; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

QY 2 NCCNGCGSSKXCRDHARC 19
II IIIII I I I I
Db 15 NCANGCQ---CGDKCEC 29

RESULT 5

H86231
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H86231
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Dwyer,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H86231
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <STO>
A:Cross-references: GB:AE005172; NID:g2160169; PIDN:AAB60732.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 42.1%; Score 51; DB 2; Length 454;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 NCCNGCGSSKXCRDHA 17
III IIII : III
Db 178 NCCRGVLTMSQDHA 193

RESULT 6

T49670
hypothetical protein B8B20.240 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C:Accession: T49670
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, May 2000
A:Reference number: 225022
A:Accession: T49670
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-147 <SCH>
A:Cross-references: EMBL:AL355933; GSPDB:GN001116; NCSP:B8B20.240
A:Experimental source: BAC clone B8B20; strain OR74A
C:Genetics:
A:Gene: NCSP:B8B20.240
A:Map position: 6
C:Superfamily: Neurospora crassa hypothetical protein B8B20.240

Query Match 41.7%; Score 50.5; DB 2; Length 147;
Best Local Similarity 42.9%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

QY 3 CCNGCGSSKXK---RDHARCC 20

Query Match 43.8%; Score 53; DB 2; Length 230;
Best Local Similarity 44.4%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 3 CCNGCGSSKXCRDHARCC 20
II: IIII I: I I
Db 120 CCSSGGSCCQ--SSCC 135

RESULT 3

S18946
ultra high-sulfur keratin 1 - human
N:Alternate names: UHS keratin; ultra high-sulfur matrix protein
C:Species: Homo sapiens (man)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: S18946; B36686
R:Drabant, B.; Doenecke, D.
submitted to the EMBL data Library, December 1991
A:Description: Nucleotide sequence of a Human high-sulphur keratin cDNA.
A:Reference number: S18946
A:Accession: S18946
A:Molecule type: mRNA
A:Residues: 1-169 <DRA>
A:Cross-references: EMBL:X63755; NID:g32471; PIDN:CAA45283.1; PID:g32472
R:MacKinnon, P.J.; Powell, B.C.; Rogers, G.E.
J. Cell Biol. 111, 2587-2600, 1990
A:Title: Structure and expression of genes for a class of cysteine-rich proteins of the
A:Reference number: A36686; MUID:91115951; PMID:1703541
A:Accession: B36686
A:Molecule type: DNA
A:Residues: 1-39, 'Y', 41-169 <MAC>
A:Cross-references: GB:X55293; NID:g34078; PIDN:CAA39005.1; PID:g34079
C:Genetics:
A:Gene: GDB:KRN1
A:Cross-references: GDB:l25257; OMIM:148021
A:Map position: 11q13-11q13
C:Superfamily: ultra-high-sulfur keratin
C:Keywords: hair; tandem repeat
F:7-15/Region: Ser-rich nonapeptide repeat
F:59-68/Region: Gly-rich decapeptide repeat
F:69-78/Region: Gly-rich decapeptide repeat
F:79-88/Region: Cys-rich decapeptide repeat
F:89-97/Region: Ser-rich nonapeptide repeat
F:98-107/Region: Cys-rich decapeptide repeat
F:108-117/Region: Cys-rich decapeptide repeat
F:118-126/Region: Ser-rich nonapeptide repeat
F:127-136/Region: Cys-rich decapeptide repeat
F:137-145/Region: Ser-rich nonapeptide repeat
F:146-155/Region: Cys-rich decapeptide repeat
F:156-165/Region: Cys-rich decapeptide repeat

Query Match 43.0%; Score 52; DB 1; Length 169;
Best Local Similarity 44.4%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 3 CCNGCGSSKXCRDHARCC 20
II: IIII I: I I
Db 87 CCSSGGSCCQ--SSCC 102

RESULT 4

A34484
metallothionein I - yeast (Candida glabrata)
C:Species: Candida glabrata
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
C:Accession: A34484
R:Whehra, R.K.; Garey, J.R.; Butt, T.R.; Gray, W.R.; Winge, D.R.
J. Biol. Chem. 264, 19747-19753, 1989
A:Title: Candida glabrata metallothioneins. Cloning and sequence of the genes and charac
A:Reference number: A92737; MUID:90062075; PMID:2584191
A:Accession: A34484
A:Molecule type: DNA

```

Db      ||:| |||: |||
30 CCHGPCSSRRAPTSPRTRCC 50

```

DEFINITION 7

T46722
 conserved hypothetical protein [imported] - Leishmania major
 N:Alternate names: probable proline synthetase associated protein
 C:Species: Leishmania major
 C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
 C:Accession: T46722
 R:K.Voickaert, G.; Ivens, A.C.; Lawson, D.; Quail, M.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, December 1999
 A:Reference number: Z23137
 A:Accession: T46722
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-389 <VOL>
 A:Cross-references: EMBL:AL121861; PIDN:CAB58387.1
 A:Experimental source: strain Friedlin
 C:Genetics:
 A:Note: L4326.11

Query Match 41.3%; Score 50; DB 2; Length 389;
Best Local Similarity 44.4%; Pred. No. 41;
Matches 8; Conservative 1; Mismatches 5; Indels 4; Gaps 1;

Qy 3 CCNGGCSKXCRDHARCC 20
11: 11 1 1 11
Db 78 CCSAGC---CLCHVDCC 91

DEC 11 9

KHRZOB
 Oryzain (BC 3.4.22.-) beta precursor - rice
 C:Species: *Oryza sativa* (rice)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jun-2000
 C:Accession: J00389; BA0053
 R:Watanabe, H.; Abe, K.; Emori, Y.; Hosoyama, H.; Arai, S.
 submitted to JIPID, May 1991
 A:Reference number: J00388
 A:Accession: J00389
 A:Molecule type: mRNA
 A:Residues: 1-471 <WAT1>
 R:Watanabe, H.; Abe, K.; Emori, Y.; Hosoyama, H.; Arai, S.
 J. Biol. Chem. 266, 16897-16902, 1991
 A:Title: Molecular cloning and gibberellin-induced expression of multiple cysteine protease
 A:Reference number: A40053; PMID:1885617

Query Match	41.3%	Score 50;	DB 1;	Length 471;
Best Local Similarity	40.9%;	Pred. No. 47;		
Matches	9: Conservative	2: Mismatches	7: Indels	4: Gaps

Qy 3 CCNGGC---SSKXCRDHARCC 20
| | : | : ||
Db 407 CLVGGCCPVEGATCCKDHASCC 428

DECLASSIFIED

```

RESULT 9
S40241
C:Species: MYTILUS EDULIS (blue mussel)
C:Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text change 17-Mar-1999

```

G protein-coupled receptor - great pond snail
C:Species: *Lymnaea stagnalis* (great pond snail)
C:date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C:Accession: S40241
R:ensen, C.P.; Kesteren, E.R.; Planta, R.J.; Cox, K.; Burke, J.F.; Heerikhuizen, H.;
submitted to the EMBL data Library, June 1993
A:description: A G protein-coupled receptor with LDL-binding motifs suggests a role f
A:Reference number: S40241
A:Accession: S40241

Query Match 40.5%; Score 49; DB 2; Length 1115;
Best Local Similarity 44.4%; Pred. No. 1.1e+02;
Matches 8: Conservative 1; Mismatches 9 Indels

QY	2	NCCNGG	SSKX	CRD	HARC	19
Dp	250	NVCDGY	CDCKT	CDDE	EVC	26

DEC 11 1961

metallothionein 20-1b - blue mussel
 C:Species: Mytilus edulis (blue mussel)
 C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 17-Mar-1999
 C:Accession: S47576
 C:MacKay, E.A.; Overnelli, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; Eur. J. Biochem. 218, 183-194, 1993
 A:Title: Complete amino acid sequences of five dimeric and four monomeric forms
 A:Reference number: S39416; MUID:94062828; PMID:8243463
 A:Accession: S47576
 A:Molecule type: protein
 A:Residues: 1-71 <MAC>
 C:Superfamily: metallothionein
 C:Keywords: chelation; metal binding

Query Match 40.1%; Score 48.5; DB 2; Length 71;
Best Local Similarity 40.7%; Pred. No. 21;
Matches 11: Conservative 1; Mismatches 6; Indels

QY 2 NC-----CNGGSSKXCR--DHARC 19

7
 8
 9
 10
 11
 12
 13

RESULT 11
S39420
metallothionein 20-1a - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text change 17-Mar-1999

Qy	3	CC-----	NGGCSSKXCRDHARCC	20
Db	59	CGCGGGGGGCGCC	CCCRPRCCCC	81

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 10, 2003, 08:32:27 ; Search time 3.30435 Seconds
(without alignments)
251.041 Million cell updates/sec

Title: US-09-910-009A-211

Perfect score: 121

Sequence: 1 XNCCGGCGSSKXCRDHARC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	43.8	194	1 KRUB_HUMAN	O75690 homo sapien
2	52	43.0	169	1 KRUA_HUMAN	P26371 homo sapien
3	51.5	42.6	62	1 MT1_CANGA	P15113 candida gla
4	50	41.3	471	1 ORYB_ORYSA	P25777 oryza sativ
5	49.5	40.9	61	1 MT1A_HORSE	P02800 equus caball
6	49	40.5	1115	1 GPCR_LYMTS	P46023 lymnaea sta
7	48.5	40.1	27	1 CXM3_CONPU	P58925 conus purpu
8	48.5	40.1	71	1 MT21_MYTED	P80251 mytilus edu
9	48.5	40.1	71	1 MT22_MYTED	P80252 mytilus edu
10	48	39.7	71	1 CXO3_CONST	O9XZK2 conus stria
11	48	39.7	250	1 STC_ANGAU	P18301 anguilla au
12	48	39.7	401	1 FLIB_SALCH	O9KIV4 salmonella
13	48	39.7	401	1 FLIB_SALTY	O56106 salmonella
14	47.5	39.3	207	1 BRX1_CHICK	Q9W6D8 gallus gall
15	47	38.8	82	1 VGI3_HSV11	O00166 ictaluriid h
16	47	38.8	221	1 OAZ_MESAU	P70112 mesocricetu
17	47	38.8	1308	1 MT44_HUMAN	O9C0A0 homo sapien
18	46.5	38.4	72	1 MT14_MYTED	P80249 mytilus edu
19	46.5	38.4	72	1 MT1A_MYTED	P80246 mytilus edu
20	46.5	38.4	72	1 MT1B_MYTED	O62554 mytilus edu
21	46.5	38.4	593	1 GRN1_HUMAN	P28799 h granulin
22	46	38.0	29	1 CXOD_CONMA	Q26350 conus magus
23	46	38.0	62	1 MT2_CAEEL	P17512 caenorhabdi
24	46	38.0	170	1 CNBP_MOUSE	P53996 mus musculu
25	46	38.0	172	1 CNBP_CHICK	O42395 gallus gall
26	46	38.0	177	1 CNBP_HUMAN	P26694 homo sapien
27	46	38.0	226	1 OAZ_MOUSE	P54369 mus musculu
28	46	38.0	226	1 OAZ_RAT	P54370 rattus norv
29	46	38.0	346	1 CYSL_LYCES	P20721 lycopersico
30	46	38.0	434	1 UL43_HSV11	P10227 herpes simp
31	46	38.0	512	1 YE94_SCHPO	O13766 schizosacch
32	46	38.0	723	1 DLL1_HUMAN	O00548 homo sapien
33	45.5	37.6	72	1 MT13_MYTED	P80248 mytilus edu

34	45.5	37.6	73	1 MT_PERVI	Q9U568 perna virid
35	45.5	37.6	714	1 DLL1_RAT	P97677 rattus norv
36	45.5	37.6	722	1 DLL1_MOUSE	O61483 mus musculu
37	45	37.2	61	1 MT2_CRIGR	P02799 cricetulus
38	45	37.2	61	1 MT2_MOUSE	P02798 mus musculu
39	45	37.2	61	1 MT2_RAT	P04355 rattus norv
40	45	37.2	124	1 WFD2_HUMAN	Q14508 homo sapien
41	45	37.2	130	1 TAT_HV2RO	P04605 human immun
42	45	37.2	197	1 T4S5_HUMAN	O14894 homo sapien
43	45	37.2	262	1 TE26_TOXCA	P54190 toxocara ca
44	45	37.2	459	1 GUN1_TRIRE	P07981 trichoderma
45	45	37.2	463	1 GUN1_TRILO	Q12714 trichoderma

ALIGNMENTS

RESULT 1

KRUB_HUMAN
ID KRUB_HUMAN STANDARD; PRT: 194 AA.
AC O75690;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Keratin, ultra high-sulfur matrix protein B (UHS keratin B) (UHS KerB).
DE KerB).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99148005; PubMed=10023043;
RA Perez C., Aurio J., Gerst C., Bernard B.A., Egly J.-M.;
RT "Genomic organization and promoter characterization of two human UHS keratin genes."
RL Gene 227:137-148(1999).
CC -!- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF 6-20 kDa, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR KERATINS (40-56 kDa).
CC -!- TISSUE SPECIFICITY: CUTICLE LAYERS OF DIFFERENTIATING HAIR FOLLICLES.
CC -!- DOMAIN: MAINLY COMPOSED OF CYS-RICH (CR), GLY-RICH (GR) AND SER-RICH (SR) REPEATS.
CC -!- SIMILARITY: BELONGS TO THE UHS KERATIN FAMILY.
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CC EMBL: AJ006692; CAA07188.1;
DR HSSP; P01055; IBB1.
KW Keratin; Repeat; Multigene family.
SQ SEQUENCE 194 AA; 18094 MW; 8607B2AE906FE44A CRC64;

Query Match 43.8%; Score 53; DB 1; Length 194;
Best Local Similarity 44.4%; Pred. No. 2.3;
Matches 8; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Qy 3 CCNCGCGSSKXCRDHARC 20
||: ||: ||: ||: ||: ||:
Db 160 CCSSCGGSSCCQ--SSCC 175

RESULT 2

KRUA_HUMAN

DE Metallothionein-I.
GN MT-I
OS Candida glabrata (Yeast) (Torulopsis glabrata).
SC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN [1]
RP SEQUENCE FROM N.A.
RR MEDLINE=90062075; PubMed=2584191;
RA Mehra R.K., Garey J.R., Butt T.R., Gray W.R., Winge D.R.;
RX "Candida glabrata metallothioneins. Cloning and sequence of the genes
RT and characterization of proteins.";
RL J. Biol. Chem. 264:19747-19753(1989).
RN [2]
RP SEQUENCE OF 1-16.
RR MEDLINE=89057829; PubMed=3194392;
RA Mehra R.K., Tarbet B.E., Gray W.R., Winge D.R.;
RX "Metal-specific synthesis of two metallothioneins and gamma-glutamyl
RT peptides in Candida glabrata."
RL Proc. Natl. Acad. Sci. U.S.A. 85:8815-8819(1988).
CC -!- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
CC SEQUESTRATION OF TOXIC METAL IONS.
CC -!- INDUCTION: BOTH MT-I AND MT-II GENES ARE REGULATED BY COPPER ION
CC IN A CONCENTRATION-DEPENDENT FASHION, AND BOTH ARE INDUCIBLE BY
CC SILVER BUT NOT BY CADMIUM SALTS.
CC -!- MISCELLANEOUS: MT-I MIGHT BIND APPROXIMATELY 11-12 MOL EQ OF
CC CU(I).
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 9.
CC -----
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CC -----
CC EMBL: J05133; AAA35272.1; --
CC DR PIR: A31252; A31252.
DR PIR: A34484; A34484.
DR Metal-binding; Metal-thiolate cluster; Copper; Repeat.
FT INIT_MET 0
FT REPEAT 22 29
FT REPEAT 55 62
FT SEQUENCE 62 AA; 6243 MW; 80D768C06C44F7A1 CRC64;
SQ

Query Match 42.6%; Score 51.5; DB 1; Length 62;
Best Local Similarity 50.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

QY 2 NCNGGCGSSKXCGRDHARC 19
|| ||||| | | | | |
Db 14 NCANGGCG--CGDKCEC 28

RESULT 4
ORYB_ORYSA
ID ORYB_ORYSA STANDARD; PRT; 471 AA.
AC P25777;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Oryzain beta chain precursor (EC 3.4.22.-).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RR STRAIN=cv. Nipponbare; TISSUE=Seed;
RX MEDLINE=91358494; PubMed=1885617;
RA Watanabe H., Abe K., Emori Y., Hosoyama H., Arai S.;

RT Molecular cloning and gibberellin-induced expression of multiple
 RL cysteine proteinases of rice seeds (oryzains).";
 CC J. Biol. Chem. 266:16897-16902(1991).
 CC -!- TISSUE SPECIFICITY: EXPRESSED ONLY IN SEEDS.
 CC -!- INDUCTION: BY GIBBERELIC ACID (GA).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
 CC -----
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 CC -----

DR EMBL; D90407; BAA14403.1; -;
 DR PIR; J00389; KHRZOB.
 DR HSSP; P00785; 2ACT.
 DR MEROPS; C01.029; -;
 DR InterPro; IPR000118; Granulin.
 DR InterPro; IPR000668; Peptidase_C1.
 DR InterPro; IPR000169; SHprot_accsite.
 DR Pfam; PF00112; Peptidase_C1; 1.
 DR Pfam; PF00396; granulin; 1.
 DR PRINTS; PR00705; PAPAIN.
 DR ProDom; PD000158; Peptidase_C1; 1.
 DR SMART; SM00277; GRAN; 1.
 DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
 KW Hydrolase; Thiol protease; Zymogen; Glycoprotein; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 139 ACTIVATION PEPTIDE (POTENTIAL).
 FT CHAIN 140 471 ORYZAIN BETA CHAIN.
 FT ACT_SITE 164 164 BY SIMILARITY.
 FT ACT_SITE 301 301 BY SIMILARITY.
 FT ACT_SITE 321 321 BY SIMILARITY.
 FT DISULFID 161 204 BY SIMILARITY.
 FT DISULFID 195 237 BY SIMILARITY.
 FT DISULFID 295 346 BY SIMILARITY.
 FT CARBOHYD 340 340 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 471 AA; 50505 MW; 0BF39D33995CEBID CRC64;

Query Match 41.3%; Score 50; DB 1; Length 471;
 Best Local Similarity 40.9%; Pred. No. 11;
 Matches 9; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

OY 3 CCGGCG-----SSKXCRDHARCC 20
 Db 407 CLVWGCGCPVEGATCKDHASCC 428

RESULT 5
 ID MTIA_HORSE STANDARD; PRT; 61 AA.
 AC P02800;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Metallothionein-IA (MT-IA).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver, and Kidney;
 RA Kojima Y., Kaegi J.H.R.;
 RT "Metallothionein.";
 RL Trends Biochem. Sci. 3:90-93(1978).
 RN [2]
 RP REVISION TO 60, AND VARIANT ARG-39.

RA Kaegi J.H.R., Kojima Y.;
 RT "Chemistry and Biochemistry of metallothionein.";
 RL Experientia Suppl. 52:25-61(1987).
 CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
 CC TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
 CC GLUCOCORTICIDS.
 CC -!- SUBUNIT: MONOMER.
 CC -!- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
 CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
 CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
 CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
 CC PIR: A03277; SMH01A.
 DR HSSP; P02795; LMHU.
 DR InterPro; IPR003019; Metallothion.
 DR Pfam; PF00131; metalthio; 1.
 DR PRINTS; PR00860; MTVERTEBRATE.
 DR PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
 KW Metal-binding; Metal-thiolate cluster; Acetylation.
 FT DOMAIN 1 29 BETA.
 FT DOMAIN 30 61 ALPHA.
 FT METAL 5 5 CLUSTER B.
 FT METAL 7 7 CLUSTER B.
 FT METAL 13 13 CLUSTER B.
 FT METAL 15 15 CLUSTER B.
 FT METAL 19 19 CLUSTER B.
 FT METAL 21 21 CLUSTER B.
 FT METAL 24 24 CLUSTER B.
 FT METAL 26 26 CLUSTER B.
 FT METAL 29 29 CLUSTER B.
 FT METAL 33 33 CLUSTER A.
 FT METAL 34 34 CLUSTER A.
 FT METAL 36 36 CLUSTER A.
 FT METAL 37 37 CLUSTER A.
 FT METAL 41 41 CLUSTER A.
 FT METAL 44 44 CLUSTER A.
 FT METAL 48 48 CLUSTER A.
 FT METAL 50 50 CLUSTER A.
 FT METAL 57 57 CLUSTER A.
 FT METAL 59 59 CLUSTER A.
 FT METAL 60 60 CLUSTER A.
 FT MOD_RES 1 1 ACETYLATION.
 FT VARIANT 39 39 G -> R.
 FT VARIANT 54 54 S -> L.
 SQ SEQUENCE 61 AA; 6040 MW; 2ELB6EE3107C7353 CRC64;

Query Match 40.9%; Score 49.5; DB 1; Length 61;
 Best Local Similarity 34.6%; Pred. No. 2.6;
 Matches 9; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

OY 2 NCCNGGCS-----SKXCRDHARCC 20
 Db 35 SCCPGGCARCAOGCVCKGASDKCSCC 60

RESULT 6
 ID GPCR_LYMST STANDARD; PRT; 1115 AA.
 AC P46023;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE G-protein coupled receptor GRL101 precursor.
 OS Lymnaea stagnalis (Great pond snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora.
 OC Lymnaeidae; Lymnaea.
 OX NCBI_TaxID=6523;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CNS;

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RX MEDLINE=94255418; PubMed=8197140;
RA Tensen C.P., van Kesteren E.R., Planta R.J., Cox K.J.A., Burke J.F.,
RA van Heerikhuizen H., Vreugdenhil E.;
RT "A G protein-coupled receptor with low density lipoprotein-binding
RT motifs suggests a role for lipoproteins in G-linked signal
RT transduction.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:4816-4820(1994).
CC -!- FUNCTION: MIGHT DIRECTLY TRANSDUCE SIGNALS CARRIED BY LARGE
CC EXTRACELLULAR (LIPO)PROTEIN(COMPLEXE)S INTO NEURONAL EVENTS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN A SMALL NUMBER OF
CC NEURONS WITHIN THE CENTRAL NERVOUS SYSTEM AND TO A LESSER EXTENT
CC IN THE HEART.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- SIMILARITY: CONTAINS 12 LDL-RECEPTOR CLASS A DOMAINS.
CC -!- SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC -----
DR EMBL; Z23104; CAA80651.1; -.
DR PIR; S40241; S40241.
DR HSP; Q07954; 1CR8.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR002172; LDL_recept_A.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_Out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00001; 7tm.1; 1.
DR Pfam; PF00057; ldl_recept_a; 11.
DR Pfam; PF00560; LRR; 6.
DR Pfam; PF01462; LRRNT; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00192; LDLa; 12.
DR SMART; SM00370; LRR; 2.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 1.
DR PROSITE; PS00237; G-PROTEIN_RECEPT_FL_1; FALSE_NEG.
DR PROSITE; PS0262; G-PROTEIN_RECEPT_FL_2; 1.
DR PROSITE; PS01209; LDLRA_1; 6.
DR PROSITE; PS00068; LDLRA_2; 11.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 1115 G-PROTEIN COUPLED RECEPTOR GRL101.
FT DOMAIN 25 767 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 768 788 1 (POTENTIAL).
FT DOMAIN 789 801 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 802 822 2 (POTENTIAL).
FT DOMAIN 823 857 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 858 878 3 (POTENTIAL).
FT DOMAIN 879 887 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 888 908 4 (POTENTIAL).
FT DOMAIN 909 941 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 942 962 5 (POTENTIAL).
FT DOMAIN 963 988 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 989 1009 6 (POTENTIAL).
FT DOMAIN 1010 1017 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1018 1038 7 (POTENTIAL).
FT DOMAIN 1039 1115 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 12 X 40 AA APPROXIMATE TANDEM REPEATS
FT DOMAIN 32 523 SIMILAR TO THE LDL-RECEPTOR CLASS A.
FT DOMAIN 36 79 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 77 115 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 116 155 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 156 196 LDL-RECEPTOR CLASS A 4.

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FT DOMAIN 195 232 LDL-RECEPTOR CLASS A 5.
FT DOMAIN 231 269 LDL-RECEPTOR CLASS A 6.
FT DOMAIN 272 318 LDL-RECEPTOR CLASS A 7.
FT DOMAIN 320 363 LDL-RECEPTOR CLASS A 8.
FT DOMAIN 365 403 LDL-RECEPTOR CLASS A 9.
FT DOMAIN 404 442 LDL-RECEPTOR CLASS A 10.
FT DOMAIN 444 485 LDL-RECEPTOR CLASS A 11.
FT DOMAIN 486 525 LDL-RECEPTOR CLASS A 12.
FT REPEAT 557 579 LRR 1.
FT REPEAT 582 605 LRR 2.
FT REPEAT 607 629 LRR 3.
FT REPEAT 630 653 LRR 4.
FT REPEAT 655 677 LRR 5.
FT REPEAT 678 701 LRR 6.
FT REPEAT 703 725 LRR 7.
FT DISULFID 38 53 BY SIMILARITY.
FT DISULFID 46 66 BY SIMILARITY.
FT DISULFID 60 77 BY SIMILARITY.
FT DISULFID 79 91 BY SIMILARITY.
FT DISULFID 86 104 BY SIMILARITY.
FT DISULFID 98 113 BY SIMILARITY.
FT DISULFID 118 131 BY SIMILARITY.
FT DISULFID 138 153 BY SIMILARITY.
FT DISULFID 158 170 BY SIMILARITY.
FT DISULFID 165 183 BY SIMILARITY.
FT DISULFID 177 194 BY SIMILARITY.
FT DISULFID 202 220 BY SIMILARITY.
FT DISULFID 214 230 BY SIMILARITY.
FT DISULFID 233 245 BY SIMILARITY.
FT DISULFID 240 258 BY SIMILARITY.
FT DISULFID 252 267 BY SIMILARITY.
FT DISULFID 274 291 BY SIMILARITY.
FT DISULFID 282 304 BY SIMILARITY.
FT DISULFID 298 316 BY SIMILARITY.
FT DISULFID 322 339 BY SIMILARITY.
FT DISULFID 334 352 BY SIMILARITY.
FT DISULFID 346 361 BY SIMILARITY.
FT DISULFID 367 379 BY SIMILARITY.
FT DISULFID 374 392 BY SIMILARITY.
FT DISULFID 386 401 BY SIMILARITY.
FT DISULFID 406 418 BY SIMILARITY.
FT DISULFID 413 431 BY SIMILARITY.
FT DISULFID 425 440 BY SIMILARITY.
FT DISULFID 446 458 BY SIMILARITY.
FT DISULFID 453 474 BY SIMILARITY.
FT DISULFID 465 483 BY SIMILARITY.
FT DISULFID 488 500 BY SIMILARITY.
FT DISULFID 495 513 BY SIMILARITY.
FT DISULFID 507 523 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 318 318 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 482 482 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 502 502 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 571 571 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 618 618 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 685 685 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1115 AA; 125865 MW; E9B801297ECE356C CRC64;
Query Match 40.5%; Score 49; DB 1; Length 1115;
Best Local Similarity 44.4%; Pred. No. 27;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
QY 2 NCCNGCGSSKXCRDHARC 19
Db 250 NVCDDGYCDKTCDDDEV 267
RESULT 7
CXM3_CONPU STANDARD; PRT; 27 AA.
ID CXM3_CONPU

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AC	P80251; P80257;
AD	01-FEB-1994 (Rel. 28, Created)
DT	01-FEB-1994 (Rel. 28, Last sequence update)
DE	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Metallothionein 20-I isoforms A and B (MT-20-IB).
DE	Mytilus edulis (Blue mussel).
OC	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC	Mytiloidea; Mytilidae; Mytilus.
OX	NCBI_TaxID=6550;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=94062828; PubMed=8243463;
RA	McKay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E.,
RA	Kaegi J.H.R., Fothergill J.E.;
RT	"Complete amino acid sequences of five dimeric and four monomeric
RT	forms of metallothionein from the edible mussel Mytilus edulis.";
RL	Eur. J. Biochem. 218:183-194(1993).
CC	-!- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
CC	SEQUESTRATION OF TOXIC METAL IONS.
CC	-!- SUBUNIT: HOMODIMER.
CC	-!- INDUCTION: BY CADMIUM.
CC	-!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2
DR	PIR; S39420; S39420.
DR	InterPro; IPRO03019; Metallothion.
DR	InterPro; IPRO01008; Mtlthlion_misc.
DR	Pfam; PF00131; metalthio; 1.
DR	PRINTS; PR00875; MTMOLLUSC.
KW	Metal-binding; Metal-thiolate cluster; Cadmium.
FT	VARIANT 66 66 S->A (IN MT-20-IB).
SQ	SEQUENCE 71 AA: 6944 MW; 4FD27FE34E81654 CRC64;
Query Match	40.1%; Score 48.5; DB 1; Length 71;
Best Local Similarity	40.1%; Pred. No. 3-9;
Matches 11;	Conservative 1; Mismatches 6; Indels 9; Gaps
QY	2 NC-----CNGCSKXCR--DHARC 19 :
Dd	5 NCietNWVICGTGCGKRCRGDACK 31
RESULT 9	
MT22_MYT2	STANDARD; PRT; 71 AA.
ID	MT22_MYT2 STANDARD; PRT;
AC	P80252;
DT	01-FEB-1994 (Rel. 28, Created)
DT	01-FEB-1994 (Rel. 28, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Metallothionein 20-II (MT-20-II).
DE	Mytilus edulis (Blue mussel).
OC	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC	Mytiloidea; Mytilidae; Mytilus.
OX	NCBI_TaxID=6550;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=94062828; PubMed=8243463;
RA	McKay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E.,
RA	Kaegi J.H.R., Fothergill J.E.;
RT	"Complete amino acid sequences of five dimeric and four monomeric
RT	forms of metallothionein from the edible mussel Mytilus edulis.";
RL	Eur. J. Biochem. 218:183-194(1993).
RN	[2]
RP	SEQUENCE FROM N.A.
PC	TISSUE=Digestive gland;
RX	MEDLINE=99206055; PubMed=10190057;
RA	Barsley D., White K.N., Lovejoy D.A.;
RT	"Cloning and characterization of metallothionein cDNAs in the mussel
RT	Mytilus edulis L. digestive gland.";
RL	Comp. Biochem. Physiol. 122C:287-296(1999).
CC	-!- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
CC	SEQUESTRATION OF TOXIC METAL IONS.
CC	-!- SUBUNIT: HOMODIMER.
CC	-!- INDUCTION: BY CADMIUM.
CC	-!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2

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DR EMBL; AJ005456; CAA06553.1; -
 DR PIR; S39421; S39421.
 DR InterPro; IPR003019; Metallthion.
 DR InterPro; IPR001008; Metlthion_misc.
 DR Pfam; PF00131; metalthio; 1.
 DR PRINTS; PR00875; MTMOLLUSC.
 KW Metal-binding; Metal-thiolate cluster; Cadmium.
 FT INIT_MET 0
 SQ SEQUENCE 71 AA; 6887 MW; 4FD275FE39857654 CRC64;

Query Match 40.1%; Score 48.5; DB 1; Length 71;
 Best Local Similarity 40.7%; Pred. No. 3.9;
 Matches 11; Conservative 1; Mismatches 6; Indels 9; Gaps 2;

QY 2 NC-----CNGGSSKXCR-DHARC 19
 || | ||| | | | | | |
 DB 5 NCIEITNVCICGTGCGKCCRCGDAKC 31

RESULT 10
 CX03_CONST
 ID CX03_CONST STANDARD; PRT; 71 AA.
 AC Q9XK2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Omega-type conotoxin S03 precursor.
 GN S03.
 OS Conus striatus (Striated cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6493;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom duct;
 RX MEDLINE=20037955; PubMed=10573284;
 RA Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
 RT "Conopeptides from Conus striatus and Conus textile by cDNA
 cloning".
 RL Peptides 20:1139-1144(1999).
 CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 CC and block voltage-sensitive calcium channels (VSOC) (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
 CC FAMILY.

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DR EMBL; AF146348; AAD31908.1; -
 DR HSP; P05484; 1LWI.
 DR InterPro; IPR004214; Conotoxin.
 DR Pfam; PF02950; Conotoxin; 1.
 KW Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
 FT SIGNAL; Amidation.
 FT SIGNAL 1 22 POTENTIAL.
 FT PROPEP 23 44 POTENTIAL.

FT PEPTIDE 45 70 OMEGA-TYPE CONOTOXIN S03.
 FT DISULFID 46 61 BY SIMILARITY.
 FT DISULFID 53 65 BY SIMILARITY.
 FT DISULFID 60 70 BY SIMILARITY.
 FT MOD_RES 70 70 AMIDATION (G-71 PROVIDE AMIDE GROUP)
 FT (POTENTIAL).
 SQ SEQUENCE 71 AA; 7628 MW; CE7070DCE3094D73 CRC64;

Query Match 39.7%; Score 48; DB 1; Length 71;
 Best Local Similarity 58.3%; Pred. No. 4.5;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 NCCNGGSSKXKC 13
 ||| | | | |
 DB 59 NCCTGSCRSKGC 70

RESULT 11
 STC_ANGAU
 ID STC_ANGAU STANDARD; PRT; 250 AA.
 AC P18301;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Stanniocalcin precursor (STC) (Corpuscles of stannius protein) (CS)
 DE (Hypocalcin) (Teleocalcin).
 GN STC.
 OS Anguilla australis (Australian eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 OC Anguilla.
 OX NCBI_TaxID=7940;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 33-57.
 RX MEDLINE=88083961; PubMed=3319739;
 RA Butkus A., Roche P.J., Fernley R.T., Haralambidis J., Coghlan J.P.;
 RA Fenschow J.D., Ryan G.B., Trahair J.F., Tregear G.W., Coghlan J.P.;
 RT "Purification and cloning of a corpuscles of Stannius protein from
 RT Anguilla australis".
 RL Mol. Cell. Endocrinol. 54:123-133(1987).
 RN [2]
 RP REVISIONS.

RA Roche P.J.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: ITS PRIMARY FUNCTION IS THE PREVENTION OF HYPERCALCEMIA.
 CC UPON RELEASE INTO THE CIRCULATION, IT LOWERS CALCIUM TRANSPORT BY
 CC THE GILLS, THEREBY REDUCING ITS RATE OF INFUX FROM THE
 CC ENVIRONMENT INTO THE EXTRACELLULAR COMPARTMENT. STC ALSO
 CC STIMULATES PHOSPHATE REABSORPTION BY RENAL PROXIMAL TUBULES. THE
 CC CONSEQUENCE OF THIS ACTION IS INCREASED LEVELS OF PLASMA
 CC PHOSPHATE, WHICH COMBINES WITH EXCESS CALCIUM AND PROMOTES ITS
 CC DISPOSAL INTO BONE AND SCALES.
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -!- TISSUE SPECIFICITY: CORPUSCLES OF STANNIUS.
 CC -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.

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DR EMBL; M36967; AAB91483.1; -
 DR PIR; A54648; A54648.
 DR InterPro; IPR004978; Stanniocalcin.
 DR Pfam; PF03298; Stanniocalcin; 1.
 KW Hormone; Signal; Glycoprotein.
 FT SIGNAL 1 17 POTENTIAL.
 FT PROPEP 18 32 POTENTIAL.
 FT CHAIN 33 250 STANNIOCALCIN.
 FT DISULFID 44 58 BY SIMILARITY.

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FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 64 113 BY SIMILARITY.
FT DISULFID 97 127 BY SIMILARITY.
FT DISULFID 134 169 BY SIMILARITY.
FT DISULFID 201 201 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 61 61 N-LINKED (GLCNAC... ) (PROBABLE).
SQ SEQUENCE 250 AA; 27174 MW; BB972BD951F75B3E CRC64;

Query Match 39.7%; Score 48; DB 1; Length 250;
Best Local Similarity 42.9%; Pred. No. 12;
Matches 9; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

QY 3 CCNG-----GCSKXCRDHARC 19
  ||| ||| | | | |
Db 44 CLNGALQVGCSAFACLDNSTC 64

RESULT 12
FLIB_SALCH
ID FLIB_SALCH STANDARD; PRT; 401 AA.
AC Q9KJ4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lysine-N-methylase (EC 2.1.1.-) (Lysine N-methyltransferase).
GN FLIB OR FLIU.
OS Salmonella cholerae-suis (Salmonella enterica).
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CH12440 / Serotype C1;
RX MEDLINE=21022014; PubMed=11142406;
RA Ho K.C., Chang G.N.;
RT "The fliu and fliv genes are expressed as a single ORF in Salmonella choleraesuis."
RL Can. J. Microbiol. 46:1149-1152(2000).
CC -!- FUNCTION: Post-translationally modifies flagellin by methylation of epsilon amino group of surface-exposed lysine residues (By similarity).
CC -!- SIMILARITY: BELONGS TO THE FLIB FAMILY.
CC -----
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CC -----
DR EMBL; AF159460; AAF80753.1; -
DR EMBL; AF159460; AAF80753.1; -
KW Transferase; Methyltransferase.
SQ SEQUENCE 401 AA; 45366 MW; C42D82DF67EDBD10 CRC64;

Query Match 39.7%; Score 48; DB 1; Length 401;
Best Local Similarity 61.5%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 8 CSSKXCRDHARC 20
  ||| ||| ||
Db 17 CSGSACRDH--CC 27

RESULT 13
FLIB_SALTY
ID FLIB_SALTY STANDARD; PRT; 401 AA.
AC Q56106; Q56087;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lysine-N-methylase (EC 2.1.1.-) (Lysine N-methyltransferase).
GN FLIB OR NML OR STM1959.

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OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / ATCC 23564, and 168-94;
RX MEDLINE=97311993; PubMed=9168604;
RA Burnens A.P., Stanley J., Sack R., Hunziker P., Brodard I., Nicolet J.;
RT "The flagellin N-methylase gene flib and an adjacent serovar-specific IS200 element in Salmonella typhimurium."
RL Microbiology 143:1539-1547(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2."
RL Nature 413:852-856(2001).
CC -!- FUNCTION: Post-translationally modifies flagellin by methylation of epsilon amino group of surface-exposed lysine residues.
CC -!- SIMILARITY: BELONGS TO THE FLIB FAMILY.
CC -----
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CC -----
DR EMBL; 254217; CAA90951.1; -
DR EMBL; 267749; CAA91562.1; -
DR EMBL; AE008787; AAL20870.1; -
DR StyGene; SG10575; flib.
KW Transferase; Methyltransferase; Complete proteome.
SQ SEQUENCE 401 AA; 45414 MW; C3CAB7A8E3C9F563 CRC64;

Query Match 39.7%; Score 48; DB 1; Length 401;
Best Local Similarity 61.5%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 8 CSSKXCRDHARC 20
  ||| ||| ||
Db 17 CSGSACRDH--CC 27

RESULT 14
BRX1_CHICK
ID BRX1_CHICK STANDARD; PRT; 207 AA.
AC Q9W6D8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein BarH-like 1 (Fragment).
GN BRX1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99228399; PubMed=10213385;
RA Barlow A.J., Bogardi J.P., Lader R., Francis-West P.H.;
RT "Expression of chick Barx-1 and its differential regulation by FGF-8 and BMP signaling in the maxillary primordia."

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Dev. Dyn. 214:291-302(1999).

-1- FUNCTION: TRANSCRIPTION FACTOR, WHICH MAY BE INVOLVED IN CRANIOFACIAL DEVELOPMENT, IN ONTOGENESIS AND IN STOMACH ORGANOGESIS. MAY HAVE A ROLE IN THE DIFFERENTIATION OF MOLARS FROM INCISORS. BINDS TO A REGULATORY MODULE OF THE NCAM PROMOTER.

-1- SUBCELLULAR LOCATION: Nuclear (Probable).

-1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE FACIAL PRIMORDIA, DEVELOPING STOMACH, AND PROXIMAL LIMBS.

-1- DEVELOPMENTAL STAGE: FIRST DETECTABLE IN THE FACIAL PRIMORDIA AT STAGE 18 AFTER NEURAL CREST MIGRATION. EXPRESSED IN REGIONS DERIVED FROM BOTH MID- AND HINDRAIN NEURAL CREST. ALSO EXPRESSED IN THE DEVELOPING CARTILAGE ELEMENTS OF THE LIMB, FIRST WITHIN A RESTRICTED POPULATION IN THE PRECHONDROGENIC MESENCHYME AND LATER IN THE ROUNDED CHONDROCYTES AT THE EPIPHYSES OF DEVELOPING LONG BONES.

-1- SIMILARITY: BELONGS TO THE BAR HOMEBOX FAMILY.

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EMBL; AF116460; AAD21043.1; -

HSSP; P14653; 1B72.

TRANSFAC; T03934; -

InterPro; IPR000047; HTH_repressr.

InterPro; IPR001356; Homeobox.

Pfam; PF00046; homeobox; 1.

PRINTS; PR00024; HOMEBOX.

PRINTS; PR00031; HTHREPRESSR.

ProDom; PD000010; Homeobox; 1.

SMART; SM00389; HOX; 1.

PROSITE; PS00027; HOMEBOX_1; 1.

PROSITE; PS00071; HOMEBOX_2; 1.

Homeobox; Transcription; DNA-binding; Nuclear protein.

NON_TER 1

DNA_BIND 95 154 HOMEBOX.

SEQUENCE 207 AA; 22467 MW; 3EDE64A91D3BCE84 CRC64;

Query Match 39.3%; Score 47.5; DB 1; Length 207;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 6 GCCSKXCRDHARCC 20
| | | | |
DB 7 GSCSSGCR---RCC 18

RESULT 15
VG13_HSV11 STANDARD; PRT; 82 AA.

AC Q00166;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical gene 13 zinc-binding protein.
GN 13.
OS Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Ictalurid Herpes-like viruses.
OX NCBI_TaxID=10401;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Auburn 1;
RX MEDLINE=92087490; PubMed=1727613;
RA Davison A.J.;
RT "Channel catfish virus: a new type of herpesvirus."
RL Virology 186:9-14(1992)
CC -----
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EMBL; M75136; AAA88194.1; -
DR EMBL; M75136; AAA88116.1; -
DR PIR; E36787; E36787.
KW Hypothetical protein; zinc; zinc-finger.
SQ SEQUENCE 82 AA; 8821 MW; 6C009A50FF8C4C67 CRC64;

Query Match 38.8%; Score 47; DB 1; Length 82;
Best Local Similarity 38.5%; Pred. No. 6.7;
Matches 10; Conservative 0; Mismatches 4; Indels 12; Gaps 2;

QY 2 NCCN-----GGCSSKXCRDHARCC 20
| | | | |
DB 10 NCCNPMSLICGGGCDLISC-----CC 30

Search completed: January 10, 2003, 08:32:58
Job time : 4.30435 secs

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OM protein - protein search, using sw model

Run on: January 10, 2003, 08:32:32 ; Search time 12 Seconds
(without alignments)
343.412 Million cell updates/sec

Title: US-09-910-009a-211

Perfect score: 121

Sequence: 1 XNCCNGGCSKXCRDHARC 20

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SP_ARCHAEA:*
- 2: SP_BACTERIA:*
- 3: SP_FUNGI:*
- 4: SP_HUMAN:*
- 5: SP_INVERTEBRATE:*
- 6: SP_MAMMAL:*
- 7: SP_MHC:*
- 8: SP_ORGANELLE:*
- 9: SP_PHAGE:*
- 10: SP_PLANT:*
- 11: SP_RODENT:*
- 12: SP_VIRUS:*
- 13: SP_VERTEBRATE:*
- 14: SP_UNCLASSIFIED:*
- 15: SP_RVIRUS:*
- 16: SP_BACTERIAP:*
- 17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56.5	46.7	550	10 Q9FEF3	Q9fef3 oryza sativ
2	54	44.6	3680	5 Q9VR08	Q9vr08 drosophila
3	53.5	44.2	48	2 Q9RFP5	Q9rfp5 mycoplasma
4	53	43.8	223	11 Q62220	Q62220 mus musculu
5	53	43.8	230	11 Q64507	Q64507 mus musculu
6	53	43.8	539	12 Q9ELT7	Q9elt7 avian infec
7	52	43.0	169	4 Q14564	Q14564 homo sapien
8	52	43.0	231	5 Q96874	Q96874 entamoeba h
9	51	42.1	162	5 Q8WSW3	Q8ws3 tetrahymena
10	51	42.1	454	10 Q04500	Q04500 arabidopsis
11	50	41.3	122	10 Q8S4X9	Q8s4x9 oryza sativ
12	50	41.3	389	5 Q9U147	Q9u147 leishmania
13	50	41.3	801	6 Q77619	Q77619 sus scrofa
14	49.5	40.9	621	13 Q8QGN9	Q8qgn9 brachydanio
15	49.5	40.9	1245	3 Q9V7V5	Q9v7v5 trichoderma
16	49	40.5	66	5 Q9N6F7	Q9n6f7 conus catus

17	49	40.5	186	16 Q8XR01	Q8xr01 ralstonia s
18	49	40.5	271	5 Q9VU12	Q9vu12 drosophila
19	49	40.5	353	13 Q90WM1	Q90wm1 rana catesb
20	49	40.5	466	10 Q9ST61	Q9st61 solanum tub
21	49	40.5	471	10 Q8S289	Q8s289 oryza sativ
22	48.5	40.1	152	5 Q9XVX3	Q9xvx3 caenorhabdi
23	48.5	40.1	164	5 Q22048	Q22048 caenorhabdi
24	48.5	40.1	166	5 Q95QX1	Q95qx1 caenorhabdi
25	48.5	40.1	191	4 Q9BYQ8	Q9byq8 homo sapien
26	48.5	40.1	197	5 Q17641	Q17641 caenorhabdi
27	48.5	40.1	210	4 Q9BYR0	Q9byr0 homo sapien
28	48.5	40.1	493	10 Q22499	Q22499 zea mays (m
29	48	39.7	66	5 Q9N6N6	Q9n6n6 conus stria
30	48	39.7	66	5 Q9NCV4	Q9ncv4 conus stria
31	48	39.7	66	5 Q9NCV3	Q9ncv3 conus stria
32	48	39.7	66	5 Q9NCV2	Q9ncv2 conus stria
33	48	39.7	66	5 Q9NCV1	Q9ncv1 conus stria
34	48	39.7	66	5 Q9NCV0	Q9ncv0 conus stria
35	48	39.7	66	5 Q9NCU1	Q9ncu1 conus stria
36	48	39.7	1372	5 Q91526	Q91526 caenorhabdi
37	47	38.8	188	5 Q18238	Q18238 caenorhabdi
38	47	38.8	188	11 Q70148	Q70148 rattus norv
39	47	38.8	353	13 Q90WM0	Q90wm0 bufo japoni
40	47	38.8	379	11 Q9JX11	Q9jx11 rattus norv
41	47	38.8	464	10 Q41064	Q41064 pisum sativ
42	47	38.8	626	10 Q9AVE7	Q9ave7 oryza sativ
43	47	38.8	1297	5 Q26632	Q26632 strongyloce
44	47	38.8	1311	4 Q8WX98	Q8wx98 homo sapien
45	47	38.8	1833	11 Q08999	Q08999 mus musculu

ALIGNMENTS

RESULT 1

Q9FEF3 ID Q9FEF3 PRELIMINARY; PRT; 550 AA.
AC Q9FEF3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE P0688A04.4 protein (P0006C01.19 protein).
GN P0688A04.4 OR P0006C01.19.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0688A04.4";
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0006C01.19";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AP002839; BAB19098.1;
DR EMBL: AP002744; BAB19077.1;
SQ SEQUENCE 550 AA; 60263 MW; 1DE6F1BBA8B9E8A1 CRC64;

Query Match 46.7%; Score 56.5; DB 10; Length 550;
Best Local Similarity 52.9%; Pred. No. 0.58;
Matches 9; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 3 CCNGGCSKXCRDHARC 19

|| |||| : ||

Db 291 CC-GGCSDRCKGRRRC 306

RESULT 2
 ID Q9VR08 PRELIMINARY; PRT: 3680 AA.
 AC Q9VR08;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE CG15637 protein.
 DP OR CG15637.
 GN Drosophila melanogaster (Fruit fly).
 OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RC MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.B., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svarksas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhao G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AF003576; AAF51000.1; -.
 DR HSSP: P35555; 1ENN.
 DR FlyBase: FBgn000488; dp.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_CA.
 DR InterPro: IPR002603; ET.
 DR InterPro: IPR003645; FOLN.
 DR InterPro: IPR002899; WR1/EB.
 DR Pfam: PF00008; EGF; 25.
 DR ProDom: PD003573; ET; 1.
 DR SMART: SM00179; EGF_CA; 16.
 DR SMART: SM00001; EGF_like; 35.
 DR SMART: SM00274; FOLN; 5.
 DR SMART: SM00289; WR1; 2.
 DR SMART: SM00289; WR1; 2.
 Query Match 44.6%; Score 54; DB 5; Length 3680;
 Best Local Similarity 57.1%; Pred. No. 7.2;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps
 QY 6 GGCSSKXCRDHARC 19
 ||||| | : : : :
 Db 3294 GGCSSKPGGENSK 3307
 ||||| | : : : :
 RESULT 3
 Q9RFP5 PRELIMINARY; PRT: 48 AA.
 AC Q9RFP5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE OrfE2.
 OS Mycoplasma fermentans.
 OC Bacteria; Firmicutes; Bacilli; Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2115;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PG18;
 RC MEDLINE=99115554; PubMed=9916088;
 RA Calcutt M.J., Kim M.F., Karpas A.B., Muhlrad P.F., Wise K.S.;
 RT "Differential posttranslational processing confers intraspecies
 RT variation of a major surface lipoprotein and a macrophage-activating
 RT lipopeptide of *Mycoplasma fermentans*.";
 RL Infect. Immun. 67:760-771(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PG18;
 RC MEDLINE=20069643; PubMed=10601219;
 RA Calcutt M.J., Lavrarr J.L., Wise K.S.;
 RT "IS1630 of *Mycoplasma fermentans*, a novel IS30-type insertion element
 RT that targets and duplicates inverted repeats of variable length and
 RT sequence during insertion.";
 RL J. Bacteriol. 181:7597-7607(1999).
 DR EMBL: AF179376; AAF15567.1; -.
 SQ SEQUENCE 48 AA; 5319 MW; 668836FA3592B2C7 CRC64;
 Query Match 44.2%; Score 53.5; DB 2; Length 48;
 Best Local Similarity 42.1%; Pred. No. 0.21;
 Matches 8; Conservative 3; Mismatches 7; Indels 1; Gaps
 QY 2 NCCNGGSSKXCRDHARC 20
 : : : : : : : : : :
 Db 31 SCCSSCKEK-CRCKCKCC 48
 : : : : : : : : : :
 RESULT 4
 Q62220 PRELIMINARY; PRT: 223 AA.
 ID Q62220
 AC Q62220;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Serine 2 ultra high sulfur protein.
 GN KSTAP5-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC STRAIN=BALB/C;
RX MEDLINE=91065960; PubMed=22500030;
RW Wood L., Mills M., Hatzenbuehler N., Vogeli G.;
RT "Serine-rich ultra high sulfur protein gene expression in murine hair
RT and skin during the hair cycle.";
RL J. Biol. Chem. 265:21375-21380(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=91154184; PubMed=1840598;
RW Wood L., Mills M., Hatzenbuehler N., Vogeli G.;
RT "Additions and Corrections: Serine-rich ultra high sulfur protein gene
RT expression in murine hair and skin during the hair cycle.";
RL J. Biol. Chem. 266:4024-4024(1991).
RD EMBL: M37760; AAA40107.1; -
DR HSSP: P01064; 1P12.
DR MGD: MGI:1354758; Krtap5-4.
DR InterPro: IPR001450; IPR04S_ferredoxin.
DR InterPro: IPR001007; VWF_C.
DR PROSITE: PS00198; 4FE4S_FERREDOXIN; UNKNOWN_2.
DR PROSITE: PS01208; VWF_C; UNKNOWN_2.
DR SEQUENCE 223 AA; 21442 MW; C654BDB9FD08C59A CRC64;
SQ
Query Match 43.8%; Score 53; DB 11; Length 223;
Best Local Similarity 44.4%; Pred. No. 0.94;
Matches 8; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Qy 3 CNGGCGSKXKRDHARC 20
||| ||| | | : ||
Db 159 CCGSGCGSCCO--SSCC 174

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RESULT 5					
ID	Q64507	PRELIMINARY;	PRT;	230 AA.	
AC	Q64507;				
DT	01-NOV-1996	(TREMBLrel. 01, Created)			
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)			
DE	Serine 1 ultra high sulfur protein.				
GN	KRTAP5-1.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BALB/C;				
RX	MEDLINE=91065960; PubMed=2250030;				
RY	Wood L., Mills M., Hatzenbuehler N., Vogeli G.;				
RT	"Serine-rich ultra high sulfur protein gene expression in murine hair				
RT	and skin during the hair cycle.";				
RL	J. Biol. Chem. 265:21375-21380(1990).				
DR	EMBL; M37759; AAA40106.1; -;				
DR	HSSP; P01064; IPT2.				
DR	MGI; M1354732; Krtap5-1.				
DR	InterPro; IPR001450; 4Pe4S_ferredoxin.				
DR	InterPro; IPR000020; Anaphylatoxin.				
DR	InterPro; IPR001305; DnaJ_CXXCXGXG.				
DR	InterPro; IPR001007; VWF-C.				
DR	PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.				
DR	PROSITE; PS01177; ANAPHYLATOXIN_1; UNKNOWN_1.				
DR	PROSITE; PS00637; DNaJ_CXXCXGXG; UNKNOWN_1.				
DR	PROSITE; PS01208; VWFC; UNKNOWN_3.				
SO	SEQUENCE 230 AA; 21781 MW; 6CC50B41B2137C23 CRC64;				
Query Match		43.8%;	Score 53;	DB 11;	Length 230;
Best Local Similarity		44.4%;	Pred. No. 0.96;		
Matches 8; Conservative			3; Mismatches 5; Indels 2;	Gaps 1;	
Qy	3	CCNGSGSSKXCRDHARC	20		
Dd	120	CCSGGGCGSSCCQ--SSCC	135		

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RESULT 6
Q9ELT7 ID Q9ELT7 PRELIMINARY; PRT; 539 AA.
AC Q9ELT7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 17, Last annotation update)
DE Surface glycoprotein S1 (Fragment).
GN S1.
OS Avian infectious bronchitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_taxID=11120;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98-07484;
RA Callison S.A., Jackwood M.W., Hilt D.A.;
RT "Genotypic characterization of foreign infectious bronchitis virus
isolates and comparison with U.S. isolates.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBDJ databases.
RR EMBL; AF288467; AAG01338.1; -
DR InterPro; IPR002551; Corona_S1.
DR Pfam; PF01600; Corona_S1; 1.
FT NON_TER 539
SQ SEQUENCE 539 AA; 58877 MW; 20189989FA13E441 CRC64;

Query Match 43.8%; Score 53; DB 12; Length 539;
Best Local Similarity 50.0%; Pred. No. 2;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

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RESULT 7
Q14564 PRELIMINARY; PRT; 169 AA.
ID Q14564;
AC Q14564;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE High-sulphur keratin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC
RC TISSUE=TESTIS;
RA Drabent B., Doenecke D.;
RT "Nucleotide sequence of a Human high-sulphur keratin cDNA.";
RL Submitted (DEC-1991) to the EMBL/GenBank/DBDJ databases.
DR EMBL; X63755; CAA45283.1;
DR HSPF; P01064; 1P12.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001138; Fungi_Trn.
DR InterPro; IPR001368; TNFR_c6.
DR InterPro; IPR001007; VWF_C.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS01208; VWF_C; UNKNOWN_2.
DR PROSITE; PS00463; ZN2_Cy6_FUNGAL_1; UNKNOWN_1.
SQ SEQUENCE 169 AA; 16216 MW; A39206EB0B49D4BE CRC64;

Query Match 43.0%; Score 52; DB 4; Length 169;
Best Local Similarity 44.4%; Pred No. 1,1;
Matches 8; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 3 CCNGCCSKXCRDHARCC 20
11: 11 1: 11

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AC 09U147;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Possible proline synthetase associated protein.
 GN L4326.11.
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Aert R., Volckaert G., Ivens A.C., Lawson D., Quail M.,
 RA Rajandream M.A., Barrell B.G.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RX MEDLINE=98146435; PubMed=9477341;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 RA Smith D.F.;
 RT "A physical map of the Leishmania major Friedlin genome.";
 RL Genome Res. 8:135-145(1998).
 DR EMBL; ALI21861; CAB58387.1; -.
 DR HSSP; P38197; IB54.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR InterPro; IPR001608; UPPF0001.
 DR Pfam; PF01168; UPPF0001; 1.
 DR TIGRFAMs; TIGR00044; UPPF0001; 1.
 DR PROSITE; PS00118; PA2_HIS; UNKNOWN_1.
 DR PROSITE; PS01211; UPPF0001; 1.
 SQ SEQUENCE 389 AA; 42606 MW; 9FA2E61700590569 CRC64;
 Query Match 41.3%; Score 50; DB 5; Length 389;
 Best Local Similarity 44.4%; Pred. No. 4.4;
 Matches 8; Conservative 1; Mismatches 5; Indels 4; Gaps 1;
 QY 3 CCNGGCSKXCRDHARCC 20
 II: II I I II
 Db 78 CCSAGC---CLCHVDCC 91
 RESULT 13
 077619
 ID 077619 PRELIMINARY; PRT; 801 AA.
 AC 077619;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Low density lipoprotein receptor (Fragment).
 GN LDLR.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=98215582; PubMed=9556295;
 RA Hasler-Rapacz J., Ellegren H., Fridolfsson A.K., Kirkpatrick B.,
 RA Kirk S., Andersson L., Rapacz J.;
 RT "Identification of a mutation in the low density lipoprotein receptor
 gene associated with recessive familial hypercholesterolemia in
 swine.";
 RL Am. J. Med. Genet. 76:379-386(1998).
 DR EMBL; AF067952; AAC39254.1; -.
 DR HSSP; P01130; IAUJ.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR000033; Ldl_receptor_rep.
 DR InterPro; IPR002172; Ldl_recept_A.
 Pfam; PF00008; EGF; 3.

DR Pfam; PF00057; ldl_recept_a; 7.
 DR Pfam; PF00058; ldl_recept_b; 5.
 DR PRINTS; PRO0261; LDLRECEPTOR.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 2.
 DR SMART; SM00192; LDLa; 7.
 DR SMART; SM00135; LY; 5.
 DR PROSITE; PS00010; ASX_HYDROXYL; 2.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS01209; LDLRA_1; 7.
 DR PROSITE; PS00068; LDLRA_2; 7.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;
 KW Lipoprotein; Receptor; Repeat.
 FT NON_TER 1
 FT NON_TER 801 801
 SQ SEQUENCE 801 AA; 88722 MW; 4D58D60CF25736A3 CRC64;
 Query Match 41.3%; Score 50; DB 6; Length 801;
 Best Local Similarity 43.5%; Pred. No. 8.1;
 Matches 10; Conservative 1; Mismatches 8; Indels 4; Gaps 1;
 QY 2 NCCNG---GCSSKXCRDHARCC 20
 : II III I I I I I I I I
 Db 63 DCENGSDDEGCSKPKTCQSDPECC 85
 RESULT 14
 080G9N
 ID 080G9N PRELIMINARY; PRT; 621 AA.
 AC 080G9N;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Granulin-A (Fragment).
 OS Brachydanio rerio (Zebrafish) (Zebrafish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cadieux B., Joly L., James S., Ekker M., Bennett H.P.J.;
 RT "Identification of Members of the Zebrafish Granulin Gene Family:
 Evidence for Two Classes Displaying Different Architectures.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF375477; AAM00265.1; -.
 FT NON_TER 621 621
 SQ SEQUENCE 621 AA; 66391 MW; F9C6331803048004 CRC64;
 Query Match 40.9%; Score 49.5; DB 13; Length 621;
 Best Local Similarity 40.9%; Pred. No. 7.8;
 Matches 9; Conservative 2; Mismatches 4; Indels 7; Gaps 2;
 QY 2 NCC---NGGCSKXCRDHARCC 20
 : II : I I I I I I I I I I
 Db 40 SCCPFHGGC-----CEDLHCC 57
 RESULT 15
 09Y7V5
 ID 09Y7V5 PRELIMINARY; PRT; 1245 AA.
 AC 09Y7V5;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Conidiospore surface protein.
 GN CMP1.
 OS Trichoderma harzianum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; mitosporic Hypocreales; Trichoderma.
 OX NCBI_TaxID=5544;
 RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 32173;
RX MEDLINE=99343881; PubMed=10413618;
RA Puyesky M., Benhamou N., Ponce Noyola P., Bauw G., Ziv T.,
RA Van Montagu M., Herrera Estrella A., Horwitz B.A.; a multidomain
RT "Developmental regulation of cmpl, a gene encoding a multidomain
RL Conidiospore surface protein of Trichoderma.";
RL Fungal Genet. Biol. 27:88-99(1999).
DR EMBL; AJ133651; CAB40845.1; -.
DR HSSP; P01180; INPO.
DR InterPro; IPR001832; Claudin.
DR InterPro; IPR001673; S_mold_repeat.
DR ProDom; PD006869; S_mold_repeat; 2.
DR PROSITE; PS01346; CLAUDIN; UNKNOWN_1.
SQ SEQUENCE 1245 AA; 135824 MW; 3249C749AFA0CDF8 CRC64;

Query Match 40.9%; Score 49.5; DB 3; Length 1245;
Best Local Similarity 45.0%; Pred. No. 14;
Matches 9; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

QY 3 CCNGGCSK--XCRDHARC 19
|.|.|.|.|.|.|.|.|.|.|.|.|.|.
Db 497 CFDGCSKSKENKCRDNRQC 516

Search completed: January 10, 2003, 08:37:37
Job time : 14 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: January 10, 2003, 08:32:27 ; Search time 3.30435 seconds
(without alignments)
251.041 Million cell updates/sec

Title: us-09-910-009a-432

Perfect score: 134

Sequence: 1 ZNCCNGCGSSKWCARDHARCC 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	39.6	194	1 KRUB_HUMAN	Q75690 homo sapien
2	52	38.8	169	1 KRUA_HUMAN	P26371 homo sapien
3	51.5	38.4	62	1 MT1_CANGA	P15113 candida gla
4	50.5	37.7	591	1 GRN_CAVPO	P28797 cavia porce
5	50	37.3	471	1 ORXB_ORYSA	P25777 oryza sativ
6	50	37.3	1115	1 GPCR_LYMST	P46023 lymnaea sta
7	48.5	36.2	61	1 MT1A_HORSE	P02800 equus cabal
8	48.5	36.2	71	1 MT21_MYTE	P80251 mytilus edu
9	48.5	36.2	71	1 MT22_MYTE	P80252 mytilus edu
10	48	35.8	76	1 CXO5_CONTE	Q9X212 conus texti
11	48	35.8	476	1 HGDA_ACIFE	P11569 acidaminoco
12	48	35.8	695	1 OXLA_NEUCR	P23623 neurospora
13	47.5	35.4	27	1 XMX3_CONPU	P58925 conus purpu
14	47.5	35.4	1172	1 AHM2_ARATH	O64474 arabidopsis
15	47	35.1	115	1 ALK1_PIG	P22298 sus scrofa
16	47	35.1	1403	1 BRL1_HUMAN	Q13075 homo sapien
17	46.5	34.7	207	1 BRXL_CHICK	Q9W608 gallus gall
18	46.5	34.7	593	1 GRN_HUMAN	P28799 h granulin
19	46	34.3	62	1 MT2_CAEEL	P17512 caenorhabdi
20	46	34.3	71	1 CXO3_CONST	Q9X2K2 conus stria
21	46	34.3	90	1 MSMB_STRCA	P83242 struthio ca
22	46	34.3	124	1 WFD2_HUMAN	Q14508 homo sapien
23	46	34.3	346	1 CYSL_LYCES	P20721 lycopersico
24	46	34.3	356	1 CMGA_BAGSU	P25953 bacillus su
25	46	34.3	566	1 TPA_BOVIN	Q28198 bos taurus
26	46	34.3	1308	1 CTA4_HUMAN	Q9C0A0 homo sapien
27	46	34.3	1581	1 LMG3_MOUSE	Q9R0B6 mus musculu
28	46	34.3	1587	1 LMG3_HUMAN	Q9Y0N6 homo sapien
29	45.5	34.0	72	1 MT14_MYTE	P80249 mytilus edu
30	45.5	34.0	72	1 MT1A_MYTE	P80246 mytilus edu
31	45.5	34.0	72	1 MT1B_MYTE	O62554 mytilus edu
32	45.5	34.0	81	1 TRGS_TACTR	P81281 tachypleus
33	45.5	34.0	714	1 DLL1_RAT	P97677 rattus norv

34	45.5	34.0	722	1 DLL1_MOUSE	Q61483 mus musculu
35	45	33.6	250	1 STC_ANGAU	P18301 anguilla au
36	45	33.6	262	1 TE26_TOXCA	P54190 toxocara ca
37	45	33.6	401	1 FLIB_SALCH	Q9K1V4 salmonella
38	45	33.6	401	1 FLIB_SALTY	Q56106 salmonella
39	45	33.6	552	1 MCRA_METJA	Q60391 methanococc
40	45	33.6	723	1 DLL1_HUMAN	O00548 homo sapien
41	45	33.6	732	1 DD35_CAEEL	Q9BKQ8 caenorhabdi
42	45	33.6	824	1 AD17_HUMAN	P78536 homo sapien
43	45	33.6	827	1 AD17_MOUSE	Q920F8 mus musculu
44	45	33.6	827	1 AD17_RAT	Q921K9 rattus norv
45	45	33.6	879	1 FPRP_RAT	Q62786 rattus norv

ALIGNMENTS

RESULT 1
KRUB_HUMAN
ID KRUB_HUMAN STANDARD; PRT: 194 AA.
AC Q75690;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Keratin, ultra high-sulfur matrix protein B (UHS keratin B) (UHS
DE KerB).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99148005; PubMed-10023043;
RA Perez C., Aurilio J., Gerst C., Bernard B.A., Egly J.M.;
RT "Genomic organization and promoter characterization of two human UHS
RT keratin genes.";
RL Gene 227:137-148(1999).
CC -!- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES
CC SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID
CC MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-
CC SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF
CC 6-20 kDa, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR
CC KERATINS (40-56 kDa).
CC -!- TISSUE SPECIFICITY: CUTICLE LAYERS OF DIFFERENTIATING
CC HAIR FOLLICLES.
CC -!- DOMAIN: MAINLY COMPOSED OF CYS-RICH (CR), GLY-RICH (GR) AND SER-
CC RICH (SR) REPEATS.
CC -!- SIMILARITY: BELONGS TO THE UHS KERATIN FAMILY.
CC
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CC
CC EMBL; AJ006692; CA007188.1;
CC HSSP; P01055; IBB1.
KW Keratin; Repeat; Multigene family.
SQ SEQUENCE 194 AA; 18094 MW; 8607B2AE906FE44A CRC64;

Query Match 39.6%; Score 53; DB 1; Length 194;
Best Local Similarity 44.4%; Pred. No. 3.9;
Matches 8; Conservative 3; Mismatches 5; Indels 2; Gaps 1;
Oy 3 CCNGCGSSKWCARDHARCC 20
||: ||| : ||
Db 160 CCSSCGSSCCQ---SSCC 175

RESULT 2
KRUA_HUMAN

Fri Jan 10 09:33:23 2003

us-09-910-009a-432.rsp

DE MT-I.
GN Candida glabrata (Yeast) (Torulopsis glabrata).
OS 01-AUG-1992 (Rel. 23, Created)
AC P26371; STANDARD; PRT; 169 AA.
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Keratin, ultra high-sulfur matrix protein A (UHS keratin A) (UHS
KerA).
DE KRNI OR UHSK1.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91115951; PubMed=1703541;
RA McKinnon P.J., Powell B.C., Rogers G.E.;
RT "Structure and expression of genes for a class of cysteine-rich
RT proteins of the cuticle layers of differentiating wool and hair
RT follicles";
RL J. Cell Biol. 111:2587-2600(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99148005; PubMed=10023043;
RA Perez C., Aurio J., Gerst C., Bernard B.A., Egly J.M.;
RT "Genomic organization and promoter characterization of two human UHS
RT keratin genes";
RL Gene 227:137-148(1999).
CC -!- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES
CC SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID
CC MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-
CC SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF
CC 6-20 Kda, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR
CC KERATINS (40-56 Kda).
CC -!- TISSUE SPECIFICITY: CUTICLE LAYERS OF DIFFERENTIATING
CC HAIR FOLLICLES.
CC -!- DEVELOPMENTAL STAGE: AT A LATE STAGE OF FIBER DIFFERENTIATION.
CC -!- DOMAIN: MAINLY COMPOSED OF CYS-RICH (CR), GLY-RICH (GR) AND SER-
CC RICH (SR) REPEATS.
CC -!- SIMILARITY: BELONGS TO THE UHS KERATIN FAMILY.
CC
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CC
CC EMBL; X55293; CAA39005.1; -.
CC EMBL; AJ006693; CAA07189.1; -.
CC HSSP; P01064; 1P12.
CC Genew; HGNC:6409; KRNI.
CC MIM; 148021; -.
CC Keratin; Repeat; Multigene family.
CC SEQUENCE 169 AA; 16276 MW; 21914FEED49D4AB CRC64;
Query Match 38.8%; Score 52; DB 1; Length 169;
Best Local Similarity 44.4%; Pred. No. 4.6;
Matches 8; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
QY 3 CCNGGCGSSKWCRCRHHCC 20
DB 87 CCSSGCGSCCQ--CSCC 102
RESULT 3
MTL_CANGA
ID MTL_CANGA STANDARD; PRT; 62 AA.
AC P15113;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Metallothionein-I.
GN MT-I.
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90062075; PubMed=2584191;
RA Mehra R.K., Garey J.R., Butt T.R., Gray W.R., Winge D.R.;
RT "Candida glabrata metallothioneins. Cloning and sequence of the genes
RT and characterization of proteins";
RL J. Biol. Chem. 264:19747-19753(1989).
RN [2]
RP SEQUENCE OF 1-16.
RX MEDLINE=89057829; PubMed=3194392;
RA Mehra R.K., Tarbet B.E., Gray W.R., Winge D.R.;
RT "Metal-specific synthesis of two metallothioneins and gamma-glutamyl
RT peptides in Candida glabrata";
RL Proc. Natl. Acad. Sci. U.S.A. 85:8815-8819(1988).
CC -!- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
CC SEQUESTRATION OF TOXIC METAL IONS.
CC -!- INDUCTION: BOTH MT-I AND MT-II GENES ARE REGULATED BY COPPER ION
CC IN A CONCENTRATION-DEPENDENT FASHION, AND BOTH ARE INDUCIBLE BY
CC SILVER BUT NOT BY CADMIUM SALTS.
CC -!- MISCELLANEOUS: MT-I MIGHT BIND APPROXIMATELY 11-12 MOL EQ OF
CC CU(I).
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 9.
CC
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CC
CC EMBL; J05133; AAA35272.1; -.
CC PIR; A31252; A31252.
CC PIR; A34484; A34484.
CC Metal-binding; Metal-thiolate cluster; Copper; Repeat.
KW INIT-MET 0
FT REPEAT 22 29
FT REPEAT 55 62
FT SEQUENCE 62 AA; 6243 MW; 80D768C06C4F7A1 CRC64;
Query Match 38.4%; Score 51.5; DB 1; Length 62;
Best Local Similarity 50.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 6; Indels 3; Gaps 1;
QY 2 NCCNGGCGSSKWCRCRHHCC 19
DB 14 NCANGGCGQ---CGDKCEC 28
RESULT 4
GRN_CAVPO
ID GRN_CAVPO STANDARD; PRT; 591 AA.
AC P28797;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Granulins precursor (Acrogranin) [Contains: Granulin 1; Granulin 2;
DE Granulin 3; Granulin 4; Granulin 5; Granulin 6; Granulin 7]
DE (Fragment).
GN GRN.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 4-21.
RC TISSUE-Testis;

RX MEDLINE-93228994; PubMed-8471244;
 RA Baba T., Hoff H.B. III, Nemoto H., Lee H., Orth J., Arai Y.,
 RA Gerton G.L.;
 RT "Acrogranin, an acrosomal cysteine-rich glycoprotein, is the
 RT precursor of the growth-modulating peptides, granulins, and
 RT epithelins, and is expressed in somatic as well as male germ cells.";
 RL Mol. Reprod. Dev. 34:233-243(1993).
 CC -!- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY
 CC PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.
 CC -!- TISSUE SPECIFICITY: UBIQUITOUS
 CC -!- PTM: GRANULINS ARE DISULFIDE BRIDGED.
 CC -----
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 CC -----
 CC EMBL; M86735; AAA37030.1; -
 DR InterPro: IPR000118; Granulin.
 DR Pfam: PF00396; granulin; 7.
 DR SMART: SM00277; GRAN; 6.
 DR PROSITE; PS00799; GRANULINS; 6.
 KW Cytokine; Repeat; Signal; Glycoprotein.
 FT NON_TER 1 1
 FT SIGNAL <1 3
 FT CHAIN 4 591 ACROGRANIN.
 FT PEPTIDE 253 298 GRANULIN 1.
 FT PEPTIDE 2111 2164 GRANULIN 2.
 FT PEPTIDE 206 261 GRANULIN 3.
 FT PEPTIDE 281 335 GRANULIN 4.
 FT PEPTIDE 2376 2415 GRANULIN 5.
 FT PEPTIDE 439 7494 GRANULIN 6.
 FT PEPTIDE 2518 2569 GRANULIN 7.
 FT CARBOHYD 183 183 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 591 AA: 62596 MW; EE7C9FC8F21CB8A1 CRC64;
 Query Match 37.7%; Score 50.5; DB 1; Length 591;
 Best Local Similarity 33.3%; Pred. No. 18;
 Matches 10; Conservative 1; Mismatches 8; Indels 11; Gaps 2;
 QY 1 ZNCCNGCCSSKW-----CRDHARCC 20
 Db 293 QTCCRLQ-SGKWCPCFPKAVCCEDHVC 321
 RESULT 5
 ID ORYB_ORYSA STANDARD; PRT; 471 AA.
 AC P25777;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Oryzain beta chain precursor (EC 3.4.22.-).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare; TISSUE=Seed;
 RX MEDLINE=91358494; PubMed=1885617;
 RA Watanabe H., Abe K., Emori Y., Hosoyama H., Arai S.;
 RT "Molecular cloning and gibberellin-induced expression of multiple
 RT cysteine proteinases of rice seeds (oryzains).";
 RL J. Biol. Chem. 266:16897-16902(1991).
 CC -!- TISSUE SPECIFICITY: EXPRESSED ONLY IN SEEDS.
 CC -!- INDUCTION: BY GIBBERELIC ACID (GA).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
 CC -----

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 CC -----
 CC EMBL; D90407; BAA14403.1; -
 DR PIR; J00389; KHRZOB.
 DR HSSP; P00785; 2ACT.
 DR MEROPS; C01.029; -
 DR InterPro: IPR000118; Granulin.
 DR InterPro: IPR000668; Peptidase_C1.
 DR Pfam: PF00112; Peptidase_C1; 1.
 DR Pfam: PF00396; granulin; 1.
 DR PRINTS; PR00705; PAPAIN.
 DR ProDom; PD000158; Peptidase_C1; 1.
 DR SMART; SM00277; GRAN; 1.
 DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
 KW Hydrolase; Thiol protease; Zymogen; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT PROPEP 22 139 ACTIVATION PEPTIDE (POTENTIAL).
 FT CHAIN 140 471 ORYZAIN BETA CHAIN.
 FT ACT_SITE 164 164 BY SIMILARITY.
 FT ACT_SITE 301 301 BY SIMILARITY.
 FT ACT_SITE 321 321 BY SIMILARITY.
 FT DISULFID 161 204 BY SIMILARITY.
 FT DISULFID 195 237 BY SIMILARITY.
 FT DISULFID 295 346 BY SIMILARITY.
 FT CARBOHYD 340 340 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 471 AA: 50505 MW; 0BF39D33955CEB1D CRC64;
 Query Match 37.3%; Score 50; DB 1; Length 471;
 Best Local Similarity 40.9%; Pred. No. 18;
 Matches 9; Conservative 2; Mismatches 7; Indels 4; Gaps 1;
 QY 3 CCNGGC-----SSKWCRDHARCC 20
 Db 407 CLVWCPCFVGATCKCKDHARCC 428
 RESULT 6
 ID GPCR_LYMST STANDARD; PRT; 1115 AA.
 AC P46023;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE G-protein coupled receptor GRLL01 precursor.
 OS Lymnaea stagnalis (Great pond snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Lymnaeidae; Lymnaea.
 OX NCBI_TaxID=6523;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CNS;
 RX MEDLINE=94255418; PubMed=8197140;
 RA Tensen C.P., van Kesteren E.R., Planta R.J., Cox K.J.A., Burke J.F.,
 RA van Heerikhuizen H., Vreugdenhil E.;
 RT "A G-protein-coupled receptor with low density lipoprotein-binding
 RT motifs suggests a role for lipoproteins in G-linked signal
 RT transduction.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:4816-4820(1994).
 CC -!- FUNCTION: MIGHT DIRECTLY TRANSDUCE SIGNALS CARRIED BY LARGE
 CC EXTRACELLULAR (LIPO)PROTEIN(COMPLEXE)S INTO NEURONAL EVENTS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN A SMALL NUMBER OF
 CC NEURONS WITHIN THE CENTRAL NERVOUS SYSTEM AND TO A LESSER EXTENT

Fri Jan 10 09:33:23 2003

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CC CC      IN THE HEART.
CC CC      -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC CC      -!- SIMILARITY: CONTAINS 12 LDL-RECEPTOR CLASS A DOMAINS.
CC CC      -!- SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).
CC CC      -----
CC CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC      the European Bioinformatics Institute. There are no restrictions on its
CC CC      use by non-profit institutions as long as its content is in no way
CC CC      modified and this statement is not removed. Usage by and for commercial
CC CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC      or send an email to license@isb-sib.ch).
CC CC      -----
CC CC      EMBL; Z23104; CAA80651.1; -.
CC CC      PIR; S40241; S40241.
CC CC      HSP; Q07954; 1CR8.
CC CC      InterPro; IPR000276; GPCR_Rhodpsn.
CC CC      InterPro; IPR002172; LDL_recept_A.
CC CC      InterPro; IPR001611; LRR.
CC CC      InterPro; IPR000372; LRR_Nterm.
CC CC      InterPro; IPR003592; LRR_Out.
CC CC      InterPro; IPR003591; LRR_typ.
CC CC      Pfam; PF00001; 7tm1_1.
CC CC      Pfam; PF00057; ldl_recept_a; 11.
CC CC      Pfam; PF00560; LRR; 6.
CC CC      Pfam; PF01462; LRRNT; 1.
CC CC      PRINTS; PR00237; GPCRHOPOPSN.
CC CC      PRINTS; PR00261; LDLRECEPTOR.
CC CC      SMART; SM00192; LDLA; 12.
CC CC      SMART; SM00370; LRR; 2.
CC CC      SMART; SM00013; LRR_TYP; 1.
CC CC      SMART; SM00369; LRR_TYP; 1.
CC CC      PROSITE; PS00237; G-PROTEIN_RECP_FL_1; FALSE_NEG.
CC CC      PROSITE; PS02662; G-PROTEIN_RECP_FL_2; 1.
CC CC      PROSITE; PS01209; LDLRA_1; 6.
CC CC      PROSITE; PS00068; LDLRA_2; 11.
CC CC      G-protein coupled receptor; Transmembrane; Glycoprotein; Repeat;
CC CC      Leucine-rich repeat; Signal.
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CC CC      FT TRANSMEM 14759 14799
CC CC      FT DOMAIN 14800 14840
CC CC      FT TRANSMEM 14841 14881
CC CC      FT DOMAIN 14882 14922
CC CC      FT TRANSMEM 14923 14963
CC CC      FT DOMAIN 14964 15004
CC CC      FT TRANSMEM 15005 15045
CC CC      FT DOMAIN 15046 15086
CC CC      FT TRANSMEM 15087 15127
CC CC      FT DOMAIN 15128 15168
CC CC      FT TRANSMEM 15169 15209
CC CC      FT DOMAIN 15210 15250
CC CC      FT TRANSMEM 15251 15291
CC CC      FT DOMAIN 15292 15332
CC CC      FT TRANSMEM 15333 15373
CC CC      FT DOMAIN 15374 15414
CC CC      FT TRANSMEM 15415 15455
CC CC      FT DOMAIN 15456 15496
CC CC      FT TRANSMEM 15497 15537
CC CC      FT DOMAIN 15538 15578
CC CC      FT TRANSMEM 15579 15619
CC CC      FT DOMAIN 15620 15660
CC CC      FT TRANSMEM 15661 15701
CC CC      FT DOMAIN 15702 15742
CC CC      FT TRANSMEM 15743 15783
CC CC      FT DOMAIN 15784 15824
CC CC      FT TRANSMEM 15825 15865
CC CC      FT DOMAIN 15866 15906
CC CC      FT TRANSMEM 15907 15947
CC CC      FT DOMAIN 15948 15988
CC CC      FT TRANSMEM 15989 16029
CC CC      FT DOMAIN 16030 16070
CC CC      FT TRANSMEM 16071 16111
CC CC      FT DOMAIN 16112 16152
CC CC      FT TRANSMEM 16153 16193
CC CC      FT DOMAIN 16194 16234
CC CC      FT TRANSMEM 16235 16275
CC CC      FT DOMAIN 16276 16316
CC CC      FT TRANSMEM 16317 16357
CC CC      FT DOMAIN 16358 16398
CC CC      FT TRANSMEM 16399 16439
CC CC      FT DOMAIN 16440 16480
CC CC      FT TRANSMEM 16481 16521
CC CC      FT DOMAIN 16522 16562
CC CC      FT TRANSMEM 16563 16603
CC CC      FT DOMAIN 16604 16644
CC CC      FT TRANSMEM 16645 16685
CC CC      FT DOMAIN 16686 16726
CC CC      FT TRANSMEM 16727 16767
CC CC      FT DOMAIN 16768 16808
CC CC      FT TRANSMEM 16809 16849
CC CC      FT DOMAIN 16850 16890
CC CC      FT TRANSMEM 16891 16931
CC CC      FT DOMAIN 16932 16972
CC CC      FT TRANSMEM 16973 17013
CC CC      FT DOMAIN 17014 17054
CC CC      FT TRANSMEM 17055 17095
CC CC      FT DOMAIN 17096 17136
CC CC      FT TRANSMEM 17137 17177
CC CC      FT DOMAIN 17178 17218
CC CC      FT TRANSMEM 17219 17259
CC CC      FT DOMAIN 17260 17300
CC CC      FT TRANSMEM 17301 17341
CC CC      FT DOMAIN 17342 17382
CC CC      FT TRANSMEM 17383 17423
CC CC      FT DOMAIN 17424 17464
CC CC      FT TRANSMEM 17465 17505
CC CC      FT DOMAIN 17506 17546
CC CC      FT TRANSMEM 
```

RA Kojima Y., Kaegi J.H.R.;
 RT "Metallothionein.";
 RL Trends Biochem. Sci. 3:90-93(1978).
 RN [2]
 RP REVISION TO 60, AND VARIANT ARG-39.
 RA Kaegi J.H.R., Kojima Y.;
 RT "Chemistry and biochemistry of metallothionein.";
 RL Experientia Suppl. 52:25-61(1987).
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
 CC TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
 CC GLUCOCORTICOIDES.
 CC CC
 CC -1- SUBUNIT: MONOMER.
 CC CC
 CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
 CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
 CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
 CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC CC
 CC -1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
 CC PIR: A03277; SMHOIA.
 DR HSSP: P02795; LMHU.
 DR InterPro: IPR003019; Metallthion.
 DR InterPro: IPR000006; Metallthion_vert.
 DR Pfam: PF00131; metalthio; 1.
 DR PRINTS: PR00860; MVTERTBRATE.
 DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
 KW Metal-binding; Metal-thiolate cluster; Acetylation.
 FT DOMAIN 1 29 BETA.
 FT DOMAIN 30 61 ALPHA.
 FT METAL 5 5 CLUSTER B.
 FT METAL 7 7 CLUSTER B.
 FT METAL 13 13 CLUSTER B.
 FT METAL 15 15 CLUSTER B.
 FT METAL 19 19 CLUSTER B.
 FT METAL 21 21 CLUSTER B.
 FT METAL 24 24 CLUSTER B.
 FT METAL 26 26 CLUSTER B.
 FT METAL 29 29 CLUSTER B.
 FT METAL 33 33 CLUSTER A.
 FT METAL 34 34 CLUSTER A.
 FT METAL 36 36 CLUSTER A.
 FT METAL 37 37 CLUSTER A.
 FT METAL 41 41 CLUSTER A.
 FT METAL 44 44 CLUSTER A.
 FT METAL 48 48 CLUSTER A.
 FT METAL 50 50 CLUSTER A.
 FT METAL 57 57 CLUSTER A.
 FT METAL 59 59 CLUSTER A.
 FT METAL 60 60 CLUSTER A.
 FT MOD_RES 1 1 ACETYLATION.
 FT VARIANT 39 39 G -> R.
 FT VARIANT 54 54 S -> L.
 SQ SEQUENCE 61 AA; 6040 MW; 2ELB6EE3107C7353 CRC64;

Query Match 36.2%; Score 48.5; DB 1; Length 61;
 Best Local Similarity 34.6%; Pred. No. 5.7;
 Matches 9; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 2 NCCNGGCS-----SKWCRDHARC 20
 DB 35 SCCPGGCARCAAGCVCKGASDKSCC 60

RESULT 8

MT21_MYTED
 ID MT21_MYTED STANDARD; PRT; 71 AA.
 AC P80251; P80257;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Metallothionein 20-I isoforms A and B (MT-20-IA and MT-20-IB).
 OS Mytilus edulis (Blue mussel).
 CC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;

OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94062828; PubMed=8243463;
 RA Mackay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E.,
 RT Kaegi J.H.R., Fothergill J.E.;
 RT "Complete amino acid sequences of five dimeric and four monomeric
 RT forms of metallothionein from the edible mussel Mytilus edulis.";
 RL Eur. J. Biochem. 218:183-194(1993).
 CC -1- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
 CC SEQUESTRATION OF TOXIC METAL IONS.
 CC CC
 CC -1- SUBUNIT: HOMODIMER.
 CC CC
 CC -1- INDUCTION: BY CADMIUM.
 CC CC
 CC -1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.
 CC PIR: S39420; S39420.
 DR InterPro: IPR003019; Metallthion.
 DR InterPro: IPR001008; Metallthion_misc.
 DR Pfam: PF00131; metalthio; 1.
 DR PRINTS: PR00875; MTMOLLUSC.
 KW Metal-binding; Metal-thiolate cluster; Cadmium.
 FT VARIANT 66 66 S -> A (IN MT-20-IB).
 SQ SEQUENCE 71 AA; 6944 MW; 4FD275FE34E81654 CRC64;
 Query Match 36.2%; Score 48.5; DB 1; Length 71;
 Best Local Similarity 40.7%; Pred. No. 6.4;
 Matches 11; Conservative 1; Mismatches 6; Indels 9; Gaps 2;
 QY 2 NC-----CNGGCSKWCR--DHARC 19
 DB 5 NCIEITNVCICGTGCGKCCRCGACKC 31
 RESULT 9
 MT22_MYTED
 ID MT22_MYTED STANDARD; PRT; 71 AA.
 AC P80252;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Metallothionein 20-II (MT-20-II).
 OS Mytilus edulis (Blue mussel).
 CC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94062828; PubMed=8243463;
 RA Mackay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E.,
 RT Kaegi J.H.R., Fothergill J.E.;
 RT "Complete amino acid sequences of five dimeric and four monomeric
 RT forms of metallothionein from the edible mussel Mytilus edulis.";
 RL Eur. J. Biochem. 218:183-194(1993).
 CC -1- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
 CC SEQUESTRATION OF TOXIC METAL IONS.
 CC CC
 CC -1- SUBUNIT: HOMODIMER.
 CC CC
 CC -1- INDUCTION: BY CADMIUM.
 CC CC
 CC -1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.
 CC PIR: S39420; S39420.
 DR InterPro: IPR003019; Metallthion.
 DR InterPro: IPR001008; Metallthion_misc.
 DR Pfam: PF00131; metalthio; 1.
 DR PRINTS: PR00875; MTMOLLUSC.
 KW Metal-binding; Metal-thiolate cluster; Cadmium.
 FT VARIANT 66 66 S -> A (IN MT-20-IB).
 SQ SEQUENCE 71 AA; 6944 MW; 4FD275FE34E81654 CRC64;

Query Match 36.2%; Score 48.5; DB 1; Length 71;
 Best Local Similarity 40.7%; Pred. No. 6.4;
 Matches 11; Conservative 1; Mismatches 6; Indels 9; Gaps 2;
 QY 2 NC-----CNGGCSKWCR--DHARC 19
 DB 5 NCIEITNVCICGTGCGKCCRCGACKC 31
 RESULT 9
 MT22_MYTED
 ID MT22_MYTED STANDARD; PRT; 71 AA.
 AC P80252;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Metallothionein 20-II (MT-20-II).
 OS Mytilus edulis (Blue mussel).
 CC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94062828; PubMed=8243463;
 RA Mackay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E.,
 RT Kaegi J.H.R., Fothergill J.E.;
 RT "Complete amino acid sequences of five dimeric and four monomeric
 RT forms of metallothionein from the edible mussel Mytilus edulis.";
 RL Eur. J. Biochem. 218:183-194(1993).
 CC -1- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
 CC SEQUESTRATION OF TOXIC METAL IONS.
 CC CC
 CC -1- SUBUNIT: HOMODIMER.
 CC CC
 CC -1- INDUCTION: BY CADMIUM.
 CC CC
 CC -1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.
 CC PIR: S39420; S39420.
 DR InterPro: IPR003019; Metallthion.
 DR InterPro: IPR001008; Metallthion_misc.
 DR Pfam: PF00131; metalthio; 1.
 DR PRINTS: PR00875; MTMOLLUSC.
 KW Metal-binding; Metal-thiolate cluster; Cadmium.
 FT VARIANT 66 66 S -> A (IN MT-20-IB).
 SQ SEQUENCE 71 AA; 6944 MW; 4FD275FE34E81654 CRC64;

Fri Jan 10 09:33:23 2003

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CC EMBL: AJ005456; CAA06553.1; -.
DR PIR: S39421; S39421.
DR InterPro: IPR003019; Metallthion.
DR Pfam: PF00131; metalthio; 1.
DR PRINTS: PR00875; MTMOLLUSC.
KW Metal-binding; Metal-thiolate cluster; Cadmium.
FT INIT-MET 0 0
SQ SEQUENCE 71 AA; 6887 MW; 4FD275FE39857654 CRC64;

Query Match 36.2%; Score 48.5; DB 1; Length 71;
Best Local Similarity 40.7%; Pred. No. 6.4;
Matches 11; Conservative 1; Mismatches 6; Indels 9; Gaps 2;

QY 2 NC-----CNGCGSSKWC--DHARC 19
|| | | | | | | | | | |
Db 5 NCIEIENVICGTCGCGCCRCGACKC 31

RESULT 10
CX05_CONTE STANDARD; PRT; 76 AA.
AC Q9XZL2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Omega-type conotoxin tx05 precursor.
GN TX05.
OS Conus textile (Cloth-of-gold cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6494;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=venom duct;
RX MEDLINE=20037955; PubMed=10573284;
RA Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
RT "Conopeptides from Conus striatus and Conus textile by cDNA
cloning.";
RL Peptides 20:1139-1144(1999).
CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
and block voltage-sensitive calcium channels (VSCC) (By
similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
FAMILY.
-----
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-----
CC EMBL: AF146358; AAD31918.1; -.
DR InterPro: IPR004214; Conotoxin.
DR Pfam: PF02950; Conotoxin; 1.
KW Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
Signal.
FT SIGNAL 1 22 POTENTIAL.
FT PROPEP 23 50 POTENTIAL.
FT PEPTIDE 51 76 OMEGA-TYPE CONOTOXIN TX05.
FT DISULFID 51 66 BY SIMILARITY.
FT DISULFID 58 70 BY SIMILARITY.
FT DISULFID 65 75 BY SIMILARITY.
SQ SEQUENCE 76 AA; 8582 MW; B284206F1E149B4D CRC64;

Query Match 35.8%; Score 48; DB 1; Length 76;
Best Local Similarity 46.2%; Pred. No. 7.8;
Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

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Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 ZNCCNGCCKSKWC 13
:|:|: | | |
Db 63 QNCCDCTCWFEC 75

RESULT 11
HGDA_ACIFE STANDARD; PRT; 476 AA.
ID HGDA_ACIFE
AC P11569;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE (R)-2-hydroxyglutaryl-CoA dehydratase alpha-subunit (EC 4.2.1.-).
GN HGDA.
OS Acidaminococcus fermentans.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Acidaminococcaceae;
OC Acidaminococcus.
OX NCBI_TaxID=905;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25085;
RX MEDLINE=89276363; PubMed=2659350;
RA Dutschko R., Wohlfarth G., Buckel P., Buckel W.;
RT "Cloning and sequencing of the genes of 2-hydroxyglutaryl-CoA
dehydratase from Acidaminococcus fermentans.";
RL Eur. J. Biochem. 181:741-746(1989).
RN [2]
RP SEQUENCE OF 1-33.
RX MEDLINE=88082776; PubMed=3691501;
RA Schweiger G., Dutschko R., Buckel W.;
RT "Purification of 2-hydroxyglutaryl-CoA dehydratase from
Acidaminococcus fermentans. An iron-sulfur protein.";
RL Eur. J. Biochem. 169:441-448(1987).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=20558245; PubMed=11106419;
RA Hans M., Buckel W., Bill E.;
RT "The iron-sulfur clusters in 2-hydroxyglutaryl-CoA dehydratase from
Acidaminococcus fermentans. Biochemical and spectroscopic
investigations.";
RL Eur. J. Biochem. 267:7082-7093(2000).
CC -!- FUNCTION: CATALYSES THE REVERSIBLE DEHYDRATION OF 2-
HYDROXYGLUTARYL-COA TO GLUTACONYL-COA. THIS IS A KEY STEP IN THE
FERMENTATION OF GLUTAMATE. IT IS ACTIVATED BY HGDC.
CC -!- COFACTOR: BINDS A 4FE-4S CLUSTER, FMN AND RIBOFLAVIN. REQUIRES
ATP, MAGNESIUM AND A REDUCING AGENT, SUCH AS TI(III)CITRATE, FOR
ACTIVITY.
CC -!- ENZYME REGULATION: ACTIVATED BY THE HGDC PROTEIN.
CC -!- PATHWAY: INVOLVED IN THE 2-HYDROXY-ACID PATHWAY OF AMINO
ACID FERMENATION.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
-----
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-----
CC EMBL: X14252; CAA32465.1; -.
DR PIR: S04477; DWDXAF.
KW Lyase; Iron-sulfur; 4Fe-4S; Magnesium; FMN.
FT INIT-MET 0 0
FT CONFLICT 25 25 P -> A (IN REF. 2).
SQ SEQUENCE 476 AA; 53890 MW; B7401C75EB7C4189 CRC64;

Query Match 35.8%; Score 48; DB 1; Length 476;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

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QY 3 CCNG--GCCSKWCRDHAR 18
 III I :II I II
 Db 185 CCNNICMTKWVEDIAR 202

RESULT 12
 OXLA_NEUCR
 ID OXLA_NEUCR STANDARD; PRT; 695 AA.
 AC P23623;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE L-amino acid oxidase precursor (EC 1.4.3.2) (LAO).
 GN LOX.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=74-OR23-1A;
 RX MEDLINE=91009158; PubMed=2145270;
 RA Niedermann D.M., Lerch K.;
 RT "Molecular cloning of the L-amino-acid oxidase gene from Neurospora
 crassa.";
 RL J. Biol. Chem. 265:17246-17251(1990).
 CC -!- CATALYTIC ACTIVITY: An L-amino acid + H(2)O + O(2) = a 2-oxo acid
 CC + NH(3) + H(2)O(2).
 CC -!- COFACTOR: FAD.
 CC -!- INDUCTION: BY ADDITION OF L-AMINO ACIDS AFTER NITROGEN STARVATION,
 CC BY STARVATION IN PHOSPHATE BUFFER AND BY THE ADDITION OF PROTEIN
 CC SYNTHESIS INHIBITORS, D-AMINO ACIDS, OR ATP.
 CC -----
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 CC -----
 DR EMBL; J05621; -; NOT_ANNOTATED_CDS.
 DR PIR; A38314; A38314.
 DR InterPro; IPR002937; Amino_oxidase.
 DR Pfam; PF01593; Amino_oxidase; 1.
 KW Oxidoreductase; Flavoprotein; FAD; Zymogen.
 FT PROPEP 1 129
 FT CHAIN 130 695 L-AMINO ACID OXIDASE.
 FT NP_BIND 177 206 FAD (ADP PART) (POTENTIAL).
 SQ SEQUENCE 695 AA; 76882 MW; 4B93DBBFA354B254 CRC64;
 Query Match 35.8%; Score 48; DB 1; Length 695;
 Best Local Similarity 44.4%; Pred. No. 42;
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ZNCCNGGCGSSKWCRRDHAR 18
 : I :III I I I : I
 Db 88 ENVQSGGCISAWSRANGR 105

RESULT 13
 CXM3_CONPU
 ID CXM3_CONPU STANDARD; PRT; 27 AA.
 AC P58925;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mu-conotoxin PIIIA precursor (Fragment).
 OS Conus purpurascens (purple cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=41690;
 RN [1]

RP SEQUENCE FROM N.A., SYNTHESIS, AND MUTAGENESIS.
 RC TISSUE=Venom duct;
 RX PubMed=9614224;
 RA Shon K.-J., Olivera B.M., Watkins M., Jacobsen R.B., Gray W.R.,
 RA Floresca C.Z., Cruz L.J., Hillyard D.R., Brink A., Terlau H.,
 RA Yoshikami D.;
 RT "mu-Conotoxin PIIIA, a new peptide for discriminating among
 RT tetradotoxin-sensitive Na channel subtypes.";
 RL J. Neurosci. 18:4473-4481(1998).
 RN [2]
 RP BINDING TO NEURONAL SODIUM CHANNELS.
 RX PubMed=10627583;
 RA Safo P., Rosenbaum T., Shcherbatko A., Choi D.-Y., Han E.,
 RA Toledo-Aral J.J., Olivera B.M., Brehm P., Mandel G.;
 RT "Distinction among neuronal subtypes of voltage-activated sodium
 RT channels by mu-conotoxin PIIIA.";
 RL J. Neurosci. 20:76-80(2000).
 RN [3]
 RP STRUCTURE BY NMR.
 RX PubMed=12006587;
 RA Nielsen K.J., Watson M., Adams D.J., Hammarstrom A.K., Gage P.W.,
 RA Hill J.M., Craik D.J., Thomas L., Adams D., Alewood P.F., Lewis R.J.;
 RT "Solution structure of mu-conotoxin PIIIA, a preferential inhibitor of
 RT persistent P/Q-sensitive sodium channels.";
 RL J. Biol. Chem. 277:0-0(2002).
 CC -!- FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium
 CC channel. This peptide causes flaccid paralysis in both mice and
 CC fish. It blocks reversibly rat neuronal type II channel, whereas
 CC it blocks irreversibly amphibian muscle Na+ channels (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- PTM: Exists in two forms, due to cis-trans isomerization at Hyp-8.
 CC -!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS. MU-TYPE
 CC FAMILY.
 CC Toxin; Neurotoxin; Sodium channel inhibitor; Hydroxylation; Amidation;
 KW Cleavage on pair of basic residues.
 FT NON_TER 1 1 PROBABLE.
 FT PROPEP <1 3 MU-CONOTOXIN PIIIA.
 FT PEPTIDE 4 25
 FT DISULFID 7 19
 FT DISULFID 8 24
 FT DISULFID 14 25
 FT MOD_RES 4 4
 FT MOD_RES 11 11
 FT MOD_RES 21 21
 FT MOD_RES 25 25
 FT MUTAGEN 17 17 R->A: DECREASE IN AFFINITY TO CHANNEL.
 SQ SEQUENCE 27 AA; 3224 MW; F0E19F45BC97AC13 CRC64;
 Query Match 35.4%; Score 47.5; DB 1; Length 27;
 Best Local Similarity 45.0%; Pred. No. 4.1;
 Matches 9; Conservative 2; Mismatches 6; Indels 3; Gaps 2;
 QY 3 CCN--GGCCKWCRDHARCC 20
 : I : I I I : I I I
 Db 7 CCGFKSCRSRCKPH-RCC 25

RESULT 14
 AHM2_ARATH
 ID AHM2_ARATH STANDARD; PRT; 1172 AA.
 AC O64474;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Potential cadmium/zinc-transporting ATPase 2 (EC 3.6.3.3)
 DE (EC 3.6.3.5).
 GN HMA4 OR ATG19110 OR T20K24.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

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FT TRANSMEM 681 700 POTENTIAL.
FT DOMAIN 701 1172 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 701 1172 HMA.
FT DOMAIN 1157 1169 POLY-HIS.
FT MOD_RES 401 401 PHOSPHORYLATION (BY SIMILARITY).
FT METAL 601 601 MAGNESIUM (BY SIMILARITY).
FT METAL 605 605 MAGNESIUM (BY SIMILARITY).
FT SEQUENCE 1172 AA; 127208 MW; 1E913B9450443440 CRC64;

Query Match 35.4%; Score 47.5; DB 1; Length 1172;
Best Local Similarity 36.7%; Pred. No.71;
Matches 11; Conservative 3; Mismatches 5; Indels 11; Gaps 3;

QY 1 ZNCNN---GGCSSKWCROHAR-----CC 20
: || |::|| ||| |:: ||
DB 1119 ETCKVKIPEACASK-CRDKAKRHSGKSCC 1147

RESULT 15
ALK1_PIG
ID ALK1_PIG STANDARD; PRT; 115 AA.
AC P22298;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antileukoproteinaise.
GN ALP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA MEDLINE=91155942; PubMed=2293019;
RX Farmer S.J., Fliss A.E., Simmen R.C.M.;
RT "Complementary DNA cloning and regulation of expression of the
RT messenger RNA encoding a pregnancy-associated porcine uterine protein
RT related to human antileukoproteinaise.";
RL Mol. Endocrinol. 4:1095-1104(1990).
CC -1- FUNCTION: THIS MUCOSAL SECRETORY PROTEIN MAY HAVE A SPECIFIC
CC FUNCTION DURING FETAL DEVELOPMENT.
CC -1- TISSUE SPECIFICITY: UTERUS AND LUNG.
CC -1- DEVELOPMENTAL STAGE: MAXIMAL EXPRESSION AT MID- AND LATE
CC GESTATION.
CC -1- INDUCTION: BY ESTROGEN AND PROGESTERONE; IN UTERUS.
CC -1- PTM: COMPARED TO HUMAN ALP, IT SEEMS TO LACK A CLEAVABLE
CC SIGNAL PEPTIDE.
CC -1- SIMILARITY: CONTAINS 2 WAP-TYPE DOMAINS.
CC
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M57446; AAA63446.1; -.
CC PIR; A36113; A36113.
CC HSPG; P19957; 28REL.
CC InterPro; IPR002221; WAP.
CC Pfam; PF00095; wap; 2.
CC PRINTS; PR00003; 4DISULPHCORE.
CC ProDom; PD001224; WAP; 1.
CC SMART; SM00217; WAP; 2.
CC PROSITE; PS00317; 4-DISULFIDE_CORE; 2.
CC Serine protease inhibitor; Repeat.
KW DOMAIN 8 62 TRYPSIN INHIBITORY DOMAIN.
FT DOMAIN 63 114 ELASTASE INHIBITORY DOMAIN.
FT DOMAIN 14 59 WAP 1.
FT DOMAIN 68 113 WAP 2.
FT ACT_SITE 28 28 TRYPSIN INHIBITORY SITE (PROBABLE).

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FT ACT_SITE 81 82 ELASTASE OR CHYMOTRYPSIN INHIBITORY SITE
FT DISULFID 18 47 (PROBABLE).
FT DISULFID 26 51 BY SIMILARITY.
FT DISULFID 34 46 BY SIMILARITY.
FT DISULFID 40 55 BY SIMILARITY.
FT DISULFID 72 101 BY SIMILARITY.
FT DISULFID 79 105 BY SIMILARITY.
FT DISULFID 88 100 BY SIMILARITY.
FT DISULFID 94 109 BY SIMILARITY.
SQ SEQUENCE 115 AA; 12518 MW; C8C937E997815BCF CRC64;

Query Match 35.1%; Score 47; DB 1; Length 115;
Best Local Similarity 26.3%; Pred. No. 14;
Matches 10; Conservative 3; Mismatches 7; Indels 18; Gaps 2;

OY 1 ZNCCNGG-----CSSKW-CRDHARCC 20
Db 10 ENALKGGACPPRKIVQCLRYEKPKCTSDWQCPDKKCC 47

Search completed: January 10, 2003, 08:32:59
Job time : 4.30435 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 10, 2003, 08:32:32 ; Search time 12 Seconds
(without alignments)
343.412 Million cell updates/sec

Title: US-09-910-009a-432

Perfect score: 134

Sequence: 1 ZNCCNGGSSKWRDHARCC 20

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	58	43.3	199	11 Q9D9Z9	Q9D9Z9 mus musculus
2	56	41.8	404	10 Q9FWK1	Q9FWK1 arabidopsis
3	56	41.8	442	10 Q9LJ49	Q9LJ49 arabidopsis
4	55.5	41.4	550	10 Q9FEF3	Q9FEF3 oryza sativ
5	54	40.3	188	10 Q8W3B3	Q8W3B3 oryza sativ
6	54	40.3	362	10 Q81811	Q81811 arabidopsis
7	54	40.3	452	10 Q9SRT7	Q9SRT7 arabidopsis
8	54	40.3	456	10 Q94KT8	Q94KT8 arabidopsis
9	53.5	39.9	48	2 Q9RFP5	Q9RFP5 mycoplasma
10	53.5	39.9	258	17 Q9RC60	Q9RC60 aeropyrum p
11	53	39.6	223	11 Q62220	Q62220 mus musculus
12	53	39.6	230	11 Q64507	Q64507 mus musculus
13	52.5	39.2	410	4 Q9H092	Q9H092 homo sapien
14	52.5	39.2	875	11 Q8VE19	Q8VE19 mus musculus
15	52	38.8	162	5 Q8WSW3	Q8WSW3 tetrahymena
16	52	38.8	169	4 Q14564	Q14564 homo sapien

17	52	38.8	1164	10 Q94JB5	Q94JB5 oryza sativ
18	52	38.8	3680	5 Q9VR08	Q9VR08 drosophila
19	51.5	38.4	1245	3 Q9Y7V5	Q9Y7V5 trichoderma
20	51.5	38.4	2910	11 Q55225	Q55225 mus musculus
21	51	38.1	231	5 Q96874	Q96874 entameba h
22	51	38.1	454	10 Q04500	Q04500 arabidopsis
23	51	38.1	480	2 Q9X5B7	Q9X5B7 clostridium
24	51	38.1	539	12 Q9ELT7	Q9ELT7 avian infec
25	51	38.1	801	6 Q77619	Q77619 sus scrofa
26	51	38.1	1704	5 Q94446	Q94446 chironomus
27	50.5	37.7	621	13 Q8QGN9	Q8QGN9 brachydanio
28	50	37.3	122	10 Q8S4X9	Q8S4X9 oryza sativ
29	50	37.3	367	4 Q9H769	Q9H769 homo sapien
30	50	37.3	389	5 Q9U147	Q9U147 feishmania
31	50	37.3	462	10 Q93X09	Q93X09 oryza sativ
32	49	36.6	78	5 Q9BPC1	Q9BPC1 conus tessu
33	49	36.6	115	12 Q99GR6	Q99GR6 cullex nigri
34	49	36.6	167	2 P71299	P71299 escherichia
35	49	36.6	271	5 Q9VU12	Q9VU12 drosophila
36	49	36.6	353	13 Q90WM1	Q90WM1 rana catesb
37	49	36.6	466	10 Q9ST61	Q9ST61 solanum tub
38	48.5	36.2	152	5 Q9XVX3	Q9XVX3 caenorhabdi
39	48.5	36.2	164	5 Q22048	Q22048 caenorhabdi
40	48.5	36.2	166	5 Q95QV1	Q95QV1 caenorhabdi
41	48.5	36.2	185	5 Q8WQ03	Q8WQ03 calliphora
42	48.5	36.2	197	5 Q17641	Q17641 caenorhabdi
43	48.5	36.2	404	10 Q9C7T5	Q9C7T5 arabidopsis
44	48.5	36.2	491	12 Q67467	Q67467 feline rola
45	48.5	36.2	493	10 Q22499	Q22499 zea mays (m

ALIGNMENTS

RESULT 1

Q9D9Z9 PRELIMINARY: PRT; 199 AA.
AC Q9D9Z9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 1700024J04RIK protein.
GN 1700024J04RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirln L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Willing L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RT Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK006305; BAB24517.1;
DR MGD; MGI:1919098; 1700024J04RIK.

RESULT 5	Q8W3B3	PRELIMINARY;	PRT;	188 AA.
ID	Q8W3B3			
AC	Q8W3B3;			
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	putative zinc finger protein.			
DE				
GN	OSJNEA0013008. 8.			
OS	Oryza sativa (Rice).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Ehrhartoideae; Oryzeae; Oryza.			
OX	NCBI_TaxID=4530;			
RP	[1]			
RP	SEQUENCE FROM N.A.			

RESULT 3
Q9LJ49
ID Q9LJ49 PRELIMINARY; PRT; 442 AA.
AC AC
DQ Q9LJ49;
DT DT
DD 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Phytochelatin synthetase-like protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=COLUMBIA;
RC Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S. ;
FL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=COLUMBIA;
RC MEDLINE=20363099; PubMed=10907853;
RX Nakamura Y. ;
RA RA

DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
DE	F14P3.14 protein.	
GN	F14P3.14	
OS	Arabidopsis thaliana (Mouse-ear cress).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.	
OX	NCBI_TaxID=3702;	
RI	[1]	
RN	SEQUENCE FROM N.A.	
RC	STRAIN=CV. COLUMBIA;	
RA	Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,	
RA	Renning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,	
RA	Bowman C.L., White O., Nierman W.C., Fraser C.M.;	
RT	"Arabidopsis thaliana chromosome III BAC F14P3 genomic sequence.";	
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AC009755; AAF02128.1; -	
SQ	SEQUENCE 452 AA; 51202 MW; A1A1820E0AF96227 CRC64;	
Query Match 40.3%; Score 54; DB 10; Length 452;		
Best Local Similarity 50.0%; Pred. No. 4;		
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps		
QY	2 NCCNGGSSKWC RDHA 17	
DB	135 NCCRGVLSWAQDPA 150	
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RESULT 8		
Q94KT8		
ID	Q94KT8 PRELIMINARY; PRT; 456 AA.	
AC	Q94KT8;	
DT	01-DEC-2001 (TrEMBLrel. 19, Created)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
DE	Putative glycosylphosphatidylinositol-anchored protein.	
GN	Arabidopsis thaliana (Mouse-ear cress).	
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.	
OX	NCBI_TaxID=3702;	
RI	[1]	
RN	SEQUENCE FROM N.A.	
RA	Schindelman G., Morikami A., Jung J., Baskin T.I., Carpita N.C.,	
RA	Derbyshire P., McCann M.C., Benfey P.N.;	
RT	"COBRA encodes a putative GPI-anchored protein, which is polarly	
RL	localized and necessary for oriented cell expansion in Arabidopsis.";	
RL	Genes Dev. 115:1115-1127(2001).	
DR	EMBL; AF319663; AAK56072.1; -	
SQ	SEQUENCE 456 AA; 51202 MW; 9868840C2E76D2C3 CRC64;	
Query Match 40.3%; Score 54; DB 10; Length 456;		
Best Local Similarity 50.0%; Pred. No. 4.1;		
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps		
QY	2 NCCNGGSSKWC RDHA 17	
DB	138 NCCRGVLSWAQDPA 153	
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RESULT 9		
Q9RFP5		
ID	Q9RFP5 PRELIMINARY; PRT; 48 AA.	
AC	Q9RFP5;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last annotation update)	
DE	Orf2.	
OC	Mycoplasma fermentans.	
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;	
OC	Mycoplasmataceae; Mycoplasma.	
OX	NCBI_TaxID=2115;	



Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	57	42.5	1417	4	US-08-900-230-3	Sequence 3, Appli
2	56	41.8	2211	4	US-08-738-884-1	Sequence 1, Appli
3	52.5	39.2	1400	4	US-08-630-915A-37	Sequence 37, Appl
4	52	38.8	58	1	US-08-279-058B-23	Sequence 23, Appl
5	52	38.8	58	4	US-08-828-323-23	Sequence 23, Appl
6	51	38.1	40	4	US-09-003-198A-14	Sequence 14, Appl
7	51	38.1	67	4	US-09-003-198A-16	Sequence 16, Appl
8	50.5	37.7	1345	2	US-08-977-767-3	Sequence 3, Appli
9	49	36.6	3025	6	5223423-3	Patent No. 5223423
10	48	35.8	695	4	US-09-314-242-12	Sequence 12, Appl
11	48	35.8	2088	4	US-09-548-372D-13	Sequence 13, Appl
12	48	35.8	2088	4	US-09-548-367D-13	Sequence 13, Appl
13	47.5	35.4	22	1	US-08-599-556-1	Sequence 1, Appli
14	47.5	35.4	22	5	PCT-US96-05262-2	Sequence 2, Appli
15	47.5	35.4	27	1	US-08-599-556-7	Sequence 7, Appli
16	47.5	35.4	27	5	PCT-US96-05262-12	Sequence 12, Appl
17	47.5	35.4	359	3	US-08-586-165-4	Sequence 4, Appli
18	47	35.1	50	4	US-08-975-080-26	Sequence 26, Appl
19	47	35.1	54	2	US-08-919-914B-42	Sequence 42, Appl
20	47	35.1	362	1	US-08-415-751-35	Sequence 35, Appl
21	47	35.1	1151	3	US-08-836-134-23	Sequence 23, Appl
22	47	35.1	1151	4	US-09-493-784-23	Sequence 23, Appl
23	47	35.1	1232	3	US-08-836-134-2	Sequence 2, Appli
24	47	35.1	1232	4	US-09-493-784-2	Sequence 2, Appli
25	46.5	34.7	45	4	US-08-900-230-53	Sequence 53, Appl
26	46.5	34.7	593	1	US-07-668-648-4	Sequence 4, Appli
27	46.5	34.7	593	2	US-08-429-998-4	Sequence 4, Appli

us-09-910-009a-432.ra1

Fri Jan 10 09:33:22 2003

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-630-915A-37

Query Match 39.2%; Score 52.5; DB 4; Length 1400;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 3; Gaps 1;

QY 3 CCGGCGSSKWCARDHARC 20
Db 190 CCGGCA---CTGTACCC 204
|||: |||

RESULT 4
US-08-279-058B-23
; Sequence 23, Application US/08279058B
; Patent No. 5668004
; GENERAL INFORMATION:
; APPLICANT: Michael E. O'Donnell
; TITLE OF INVENTION: DNA POLYMERASE III
; TITLE OF INVENTION: HOLOENZYME
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/279,058B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: CRF D-1056CIP
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-279-058B-23

Query Match 38.8%; Score 52; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 11;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 CNGGCGSSKWCARDHARC 20
Db 38 CTGGCTACTCGTGAACC 54
|||: |||

RESULT 5
US-08-828-323-23
; Sequence 23, Application US/08828323A
; Patent No. 6413753
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael
; TITLE OF INVENTION: DNA POLYMERASE III HOLOENZYME
; FILE REFERENCE: 19603/10214
; CURRENT APPLICATION NUMBER: US/08/828,323A
; CURRENT FILING DATE: 1997-03-28
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; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 58
; TYPE: PRF
; ORGANISM: Escherichia coli
US-08-828-323-23

Query Match 38.8%; Score 52; DB 4; Length 58;
Best Local Similarity 47.1%; Pred. No. 11;
Matches 8; Conservative 2; Mismatches 7; Indels 7; Gaps 0;

Qy 4 CNGGCSKWCGRDHACC 20
| | | | |
Db 38 CTGGCTACTCGTGAACC 54

RESULT 6
US-09-003-198A-14
; Sequence 14, Application US/09003198A
; Patent No. 6316407
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,198A
; FILING DATE: 07-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-003-198A-14

Query Match 38.1%; Score 51; DB 4; Length 40;
Best Local Similarity 40.7%; Pred. No. 10;
Matches 11; Conservative 0; Mismatches 6; Indels 10; Gaps 1;

Qy 4 CNGGCS-----SKWCRDHACC 20
| | | | |
Db 14 CFGGCDPHCKTKEHLLSGRCRDRCC 40

RESULT 7
US-09-003-198A-16
; Sequence 16, Application US/09003198A

; Patent No. 6316407
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,198A
; FILING DATE: 07-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-003-198A-16

Query Match 38.1%; Score 51; DB 4; Length 67;
Best Local Similarity 40.7%; Pred. No. 16;
Matches 11; Conservative 0; Mismatches 6; Indels 10; Gaps 1;

Qy 4 CNGGCS-----SKWCRDHACC 20
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Db 41 CFGGCDPHCKTKEHLLSGRCRDRCC 67

RESULT 8
US-08-977-767-3
; Sequence 3, Application US/08977767
; Patent No. 5972684
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Yue, Henry
; APPLICANT: Greenwald, Sara
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: CARBONIC ANHYDRASE VIII
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,767
; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0423 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1345 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1532042
; US-08-977-767-3

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Best Local Similarity 50.0%; Pred. No. 2.2e+02;
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QY 3 CCNGGCSKWCARDHARCC 20
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Db 774 CTGGCCATTC-TCAGCC 790

RESULT 9
5223423-3
; Patent No. 5223423
; APPLICANT: FRANCHINI, GENOVEFFA, WONG-STAAAL, FLOSSIE;
; GALLO, ROBERT
; TITLE OF INVENTION: CHARACTERIZATION OF REPLICATION COMPETENT
; HUMAN IMMUNODEFICIENCY TYPE 2 PROVIRAL CLONE HIV-2 SBL/ISY
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/331,212
; FILING DATE: 03-31-1989
; SEQ ID NO: 3:
; LENGTH: 3025
5223423-3

Query Match 36.6%; Score 49; DB 6; Length 3025;
Best Local Similarity 38.9%; Pred. No. 6.5e+02;
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QY 3 CCNGGCSKWCARDHARCC 20
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Db 2436 CSNSNSCWTWSRDNKKCC 2453

RESULT 10
US-09-314-242-12
; Sequence 12, Application US/09314242A
; Patent No. 6248575
; GENERAL INFORMATION:
; APPLICANT: Elizabeth J. Colighly
; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
; FILE REFERENCE: 5556.200-US
; CURRENT APPLICATION NUMBER: US/09/314,242A
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 09/080,428
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Trichoderma harzianum
US-09-314-242-12

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Best Local Similarity 44.4%; Pred. No. 2.4e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 ZNCCNGGCSKWCARDHAR 18
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Db 88 ENVQSGGCISAWSRANG 105

RESULT 11
US-09-548-372D-13
; Sequence 13, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 2088
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-13

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Best Local Similarity 44.4%; Pred. No. 6.2e+02;
Matches 8; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCNGGCSKWCARDHARCC 20
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Db 1617 CCTGGACGATCTCCAGCC 1634

RESULT 12
US-09-548-367D-13
; Sequence 13, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 13
; LENGTH: 2088
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-13

Query Match 35.8%; Score 48; DB 4; Length 2088;
Best Local Similarity 44.4%; Pred. No. 6.2e+02;
Matches 8; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 CCGGCSKWCRCRDHACC 20
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Db 1617 CTGACGATCTCCAGCC 1634

RESULT 13
US-08-599-556-1
; Sequence 1, Application US/08599556
; Patent No. 5670622

; GENERAL INFORMATION:
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Yoshikami, Doju
; APPLICANT: Marsh, Maren
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Conotoxin Peptide PIIIA
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005-3917

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,556
; FILING DATE:
; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 24260-107674-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus purpurascens

; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Amino acid 1 is pyroglutamate or glutamine."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Amino acid 8 is 4-transhydroxyproline or proline."

; FEATURE:
; NAME/KEY: Disulfide-bond

; LOCATION: 4..16
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 5..21
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 11..22
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; NAME/KEY: Modified-site
; LOCATION: 18
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; OTHER INFORMATION: /note= "Amino acid 18 is 4-transhydroxyproline or proline."
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; LOCATION: 22
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "The carboxy terminus may be amidated."
US-08-599-556-1

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Matches 9; Conservative 2; Mismatches 6; Indels 3; Gaps 2;

QY 3 CCN--GGCSSKWCRCRDHACC 20
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Db 4 CCGFKSCRSROCKXH-RCC 22

RESULT 14
PCT-US96-05262-2
; Sequence 2, Application PC/TUS9605262
; GENERAL INFORMATION:

; APPLICANT: Shon, Ki-Joon
; APPLICANT: Grille, Michelle M.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Yoshikami, Doju
; APPLICANT: Marsh, Maren
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05262
; FILING DATE: 17-APR-1996

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/423,561
; FILING DATE: 17-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 24260-107674
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

us-09-910-009a-432.ra

Fri Jan 10 09:33:22 2003

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; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus purpurascens
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; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Amino acid 1 is pyroglutamate or glutamine."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Amino acid 8 is 4-trans-hydroxyproline or proline."
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 4..16
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 5..21
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 11..22
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 18
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Amino acid 18 is 4-trans-hydroxyproline or proline."
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; LOCATION: 22
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "The carboxy terminus may be amidated."
; PCT-US96-05262-2

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Query Match 35.4%; Score 47.5; DB 5; Length 22;
Best Local Similarity 45.0%; Pred. No. 15;
Matches 9; Conservative 2; Mismatches 6; Indels 3; Gaps 2;

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QY 3 CCN--GGCSSKWCARDHARCC 20
DB 4 CCGFKKSCRSROCKXH-RCC 22

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RESULT 15
US-08-599-556-7
; Sequence 7, Application US/08599556
; Patent No. 5670622
; GENERAL INFORMATION:
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Yoshikami, Doju
; APPLICANT: Marsh, Maren
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Conotoxin Peptide PIIIA
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005-3917
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,556
; FILING DATE:
; CLASSIFICATION: 530

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; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 24260-107674-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-599-556-7

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Query Match 35.4%; Score 47.5; DB 1; Length 27;
Best Local Similarity 45.0%; Pred. No. 18;
Matches 9; Conservative 2; Mismatches 6; Indels 3; Gaps 2;

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QY 3 CCN--GGCSSKWCARDHARCC 20
DB 7 CCGFKKSCRSROCKPH-RCC 25

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Search completed: January 10, 2003, 08:38:19
Job time : 6.91304 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2003, 08:33:07 ; Search time 30.9565 Seconds
(without alignments)
12.534 Million cell updates/sec

Title: US-09-910-009A-432

Perfect score: 134
Sequence: 1 ZNCCNGGCSKWCARDHARCC 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications_AA.*
- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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 - 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	56	41.8	2211	9 US-10-096-961-1	Sequence 1, Appli
3	55	41.0	1497	10 US-09-060-854B-2	Sequence 2, Appli
4	53	39.6	32	10 US-09-894-882-470	Sequence 470, App
5	53	39.6	40	10 US-09-894-882-498	Sequence 498, App
6	53	39.6	68	10 US-09-894-882-274	Sequence 274, App
7	53	39.6	1200	10 US-09-826-508-3	Sequence 3, Appli
8	52.5	39.2	1400	10 US-09-879-957-37	Sequence 37, Appl
9	52.5	39.2	4679	10 US-09-804-898-2	Sequence 2, Appli
10	50	37.3	1743	12 US-10-052-586-451	Sequence 451, App
11	49	36.6	42	8 US-08-969-137-3	Sequence 269, App
12	49	36.6	1300	12 US-10-052-586-269	Sequence 41823, A
13	48	35.8	32	10 US-09-864-761-41823	Sequence 1494, Ap
14	47	35.1	60	9 US-09-796-692-1494	Sequence 38546, A
15	47	35.1	60	9 US-09-864-761-38546	Sequence 1921, Ap
16	47	35.1	1403	8 US-08-913-322-22	Sequence 22, Appl
17	47	35.1	1403	8 US-08-913-322-24	Sequence 24, Appl
18	47	35.1	1403	8 US-08-913-322-24	Sequence 1, Appli
19	47	35.1	1422	10 US-09-735-933-1	

20	46.5	34.7	593	9 US-09-824-647-17	Sequence 17, Appl
21	46.5	34.7	593	10 US-08-813-156-17	Sequence 17, Appl
22	46.5	34.7	593	10 US-08-824-807-17	Sequence 17, Appl
23	46.5	34.7	621	10 US-09-925-301-1416	Sequence 1416, Ap
24	46	34.3	46	10 US-09-894-882-19	Sequence 19, Appl
25	46	34.3	46	10 US-09-894-882-58	Sequence 58, Appl
26	46	34.3	46	10 US-09-894-882-105	Sequence 105, App
27	46	34.3	46	10 US-09-894-882-407	Sequence 407, App
28	46	34.3	46	10 US-09-894-882-428	Sequence 428, App
29	46	34.3	46	10 US-09-894-882-428	Sequence 428, App
30	46	34.3	48	10 US-09-894-882-431	Sequence 28, Appl
31	46	34.3	48	10 US-09-894-882-18	Sequence 18, Appl
32	46	34.3	82	10 US-09-894-882-57	Sequence 57, Appl
33	46	34.3	82	10 US-09-894-882-104	Sequence 104, App
34	46	34.3	84	10 US-09-894-882-27	Sequence 27, Appl
35	46	34.3	137	10 US-09-925-300-1361	Sequence 1361, Ap
36	46	34.3	137	10 US-09-925-300-1361	Sequence 50, Appl
37	46	34.3	252	10 US-09-764-903-50	Sequence 10, Appl
38	46	34.3	735	10 US-09-898-570-10	Sequence 12, Appl
39	46	34.3	845	10 US-09-898-570-12	Sequence 47, Appl
40	46	34.3	914	9 US-09-975-143-47	Sequence 14, Appl
41	46	34.3	974	10 US-09-898-570-14	Sequence 16, Appl
42	46	34.3	1009	10 US-09-898-570-16	Sequence 581, App
43	46	34.3	1435	12 US-10-052-586-581	Sequence 10, Appl
44	46	34.3	1587	10 US-09-845-583-10	Sequence 12, Appl
45	45.5	34.0	722	10 US-09-908-322-12	

ALIGNMENTS

RESULT 1
US-10-029-217A-24
; Sequence 24, Application US/10029217A
; Patent No. US20020164735A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC N.
; APPLICANT: WANG, DA-2HI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO A CARDIAC-SPECIFIC
; TITLE OF INVENTION: NUCLEAR REGULATORY FACTOR
; FILE REFERENCE: UTSID:695US
; CURRENT APPLICATION NUMBER: US/10/029.217A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/257,761
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 3907
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-029-217A-24

Query Match 43.3%; Score 58; DB 9; Length 3907;
Best Local Similarity 44.4%; Pred. No. 31;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
QY 3 CCNGGCSKWCARDHARCC 20
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Db 535 CCTGGCAGCAGCCTCC 552

RESULT 2
US-10-096-961-1
; Sequence 1, Application US/10096961
; Patent No. US2002015572A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al.
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000849DIV
; CURRENT APPLICATION NUMBER: US/10/096,961

us-09-910-009a-432.rapb

Fri Jan 10 09:33:22 2003

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; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/232,632
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 09/738,884
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2211
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-096-961-1

Query Match          41.8%; Score 56; DB 9; Length 2211;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

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Db 47 CCGGCTCCGCAAGATCC 64

RESULT 3
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; Sequence 2, Application US/09060854B
; Patent No. US20020081703A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David Aaron
; TITLE OF INVENTION: Human Protease and Use of Such Protease for Pharmaceutical
; TITLE OF INVENTION: Applications and for Reducing the Allergenicity of No. US2002008
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: GC532
; CURRENT APPLICATION NUMBER: US/09/060,854B
; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1497
; TYPE: PRT
; ORGANISM: B. amyloliquefaciens
US-09-060-854B-2

Query Match          41.0%; Score 55; DB 10; Length 1497;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

Qy 3 CCGGCGSSKWCGRDHARCC 20
   ||||| | | | |
Db 1017 CCGGCGTATCT--ATCC 1032

RESULT 4
US-09-894-882-470
; Sequence 470, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 498
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-498

Query Match          39.6%; Score 53; DB 10; Length 40;
Best Local Similarity 52.9%; Pred. No. 3.2;
Matches 9; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Qy 3 CCGGCGSSKWCGRDHARCC 19
   ||||| | | | |
Db 14 CCGMCCSGWCT--RRC 28

RESULT 5
US-09-894-882-498
; Sequence 498, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 498
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-498

Query Match          39.6%; Score 53; DB 10; Length 40;
Best Local Similarity 52.9%; Pred. No. 3.2;
Matches 9; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Qy 3 CCGGCGSSKWCGRDHARCC 19
   ||||| | | | |
Db 14 CCGMCCSGWCT--RRC 28

RESULT 6
US-09-894-882-274
; Sequence 274, Application US/09894882
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; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 274
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Conus virgo
; US-09-894-882-274

Query Match 39.6%; Score 53; DB 10; Length 68;
Best Local Similarity 52.9%; Pred. No. 4.8;
Matches 9; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 3 CCGGCGSSKWCGRDHRCC 19
DB 42 CCSQMCSSGWCT--RRC 56

RESULT 7
US-09-826-508-3
; Sequence 3, Application US/09826508
; Patent No. US20010025099A1
; GENERAL INFORMATION:
; APPLICANT: Nabil Elshourbagy
; APPLICANT: Lisa Vavter
; TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides
; FILE REFERENCE: GP-70744USB
; CURRENT APPLICATION NUMBER: US/09/826,508
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1200
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-826-508-3

Query Match 39.6%; Score 53; DB 10; Length 1200;
Best Local Similarity 44.4%; Pred. No. 45;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 CCGGCGSSKWCGRDHRCC 20
DB 40 CCGGCGAGGTCCCGCCC 57

RESULT 8
US-09-879-957-37
; Sequence 37, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. US20020034755Alh
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: McCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1400 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-09-879-957-37
Query Match 39.2%; Score 52.5; DB 10; Length 1400;
Best Local Similarity 50.0%; Pred. No. 58;
Matches 9; Conservative 1; Mismatches 5; Indels 3; Gaps 1;

QY 3 CCGGCGSSKWCGRDHRCC 20
DB 190 CCGGCGCA---CTGTACCC 204

RESULT 9
US-09-804-898-2
; Sequence 2, Application US/09804898
; Patent No. US20020045264A1
; GENERAL INFORMATION:
; APPLICANT: DURING, MATTHEW
; APPLICANT: XIAO, WEIDONG
; TITLE OF INVENTION: PRODUCTION OF CHIMERIC CAPSID VECTORS
; FILE REFERENCE: 102182-14
; CURRENT APPLICATION NUMBER: US/09/804,898
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/189,110
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 6

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us-09-910-009a-432.rapb

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 4679
; TYPE: PRT
; ORGANISM: adeno-associated virus 2
US-09-804-898-2

Query Match      39.2%; Score 52.5; DB 10; Length 4679;
Best Local Similarity 44.4%; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

QY 3 CCGGCGCTTTCG----CC 4633
Db 4621 CCGGCGCTTTCG----CC 4633

RESULT 10
US-10-052-586-451
; Sequence 451, Application US/10052586
; Patent No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/052,586
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/086023
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/086392
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/086486
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/087098
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087208
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087609
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087827
;; PRIOR FILING DATE: 1998-06-03
;; PRIOR APPLICATION NUMBER: 60/088025
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088038
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088029
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088033
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088167
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088202
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088212
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088326
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088655
;; PRIOR FILING DATE: 1998-06-09
;; PRIOR APPLICATION NUMBER: 60/088722
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088738
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088740
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088811
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088824
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088825
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088826
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088863
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089090
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089908

Query Match 37.3%; Score 50; DB 12; Length 1743;
Best Local Similarity 44.4%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 3 CCNGGSSKWCARDHARCC 20
|| ||| : | ||
DB 293 CCTGGCCATGCT-CTCC 308

RESULT 11

US-08-969-137-3
; Sequence 3, Application US/08969137
; Patent No. US20010018207A1
; GENERAL INFORMATION:
; APPLICANT: KANDEL, ERIC
; APPLICANT: MAYFORD, MARK
; TITLE OF INVENTION: DNA REGULATORY ELEMENT FOR THE
; EXPRESSION OF TRANSGENES IN NEURONS OF THE MOUSE FOREBRAIN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER AND DUNHAM
; STREET: 1185 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: UNITED STATES
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,137
; FILING DATE: 12-NOV-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WHITE, JOHN P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/52776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)2278821
; TELEFAX: (212)3910525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-969-137-3

Query Match 36.6%; Score 49; DB 8; Length 42;
Best Local Similarity 44.4%; Pred. No. 9.2;
Matches 8; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

QY 3 CCNGGSSKWCARDHARCC 20
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DB 9 CCAGGCAAGC---GCC 22

RESULT 12

US-10-052-586-269
; Sequence 269, Application US/10052586
; Patent No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria

us-09-910-009a-432.rapb

Fri Jan 10 09:33:22 2003

APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063564
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063734
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063870
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066120
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066466
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069425
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: 60/069870
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/068017
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
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PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-04-29
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PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-05-05
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 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089908

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 Best Local Similarity 38.9%; Pred. No. 1.4e+02;
 Matches 7; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 CNGGCSKWCARDHARCC 20
 DB 525 CCGGACATGCTGTACC 542

RESULT 13
 US-09-864-761-41823
 ; Sequence 41823, Application US/098664761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: Aecmca-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/006666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/006667
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 ; PRIOR FILING DATE: 2001-01-30
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 ; PRIOR FILING DATE: 2001-01-30
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 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 41823
 ; LENGTH: 32
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO ALL139392.1
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.7
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.6
 ; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
 US-09-864-761-41823

Query Match 35.8%; Score 48; DB 10; Length 32;
 Best Local Similarity 41.2%; Pred. No. 9.7;
 Matches 7; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 CNGGCSKWCARDHARCC 20
 DB 8 COAWCWFQWCLCHCCCC 24

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 US-09-796-692-1494
 ; Sequence 1494, Application US/09796692
 ; Publication No. US20020198362A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Mannion, Jane
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
 ; FILE REFERENCE: 2077.001200
 ; CURRENT APPLICATION NUMBER: US/09/796,692
 ; CURRENT FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: 60/186,126
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: 60/190,479
 ; PRIOR FILING DATE: 2000-03-17

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Fri Jan 10 09:33:22 2003

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; PRIOR APPLICATION NUMBER: 60/200,545
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; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1494
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(60)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-796-692-1494

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Matches 7; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 5 NGGCSKWCARDHARCC 20
DB 36 SSSCSARWCL--GRCC 49
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; III

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Query Match          35.1%; Score 47; DB 9; Length 60;
Best Local Similarity 43.8%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

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QY 5 NGGCSKWCARDHARCC 20
DB 36 SSSCSARWCL--GRCC 49
; II::II
; III

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RESULT 15
US-09-796-692-1921
; Sequence 1921, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
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; PRIOR APPLICATION NUMBER: 60/200,545
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; PRIOR APPLICATION NUMBER: 60/200,303
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; PRIOR APPLICATION NUMBER: 60/200,779
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; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903

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; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-09-745-763-77

Query Match 13.8%; Score 58; DB 10; Length 271;
Best Local Similarity 33.3%; Pred. No. 26;
Matches 21; Conservative 6; Mismatches 20; Indels 16; Gaps 5;

QY 25 LDGDQPADRP-AERMDDISSDEHPLFDKRNCCNG-----GCSSKWC---RDH---ARC 72
Db 213 VDGQGVNDRDYMERKNKIDVNE----VRSRAQCCAGCGRGLGGCGPGSACVSRSHATWARC 268

QY 73 CGR 75
Db 269 IVR 271

RESULT 13
US-09-925-301-1351
; Sequence 1351, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1351
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (299)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1351

Query Match 13.8%; Score 58; DB 10; Length 312;
Best Local Similarity 27.3%; Pred. No. 31;
Matches 15; Conservative 7; Mismatches 19; Indels 14; Gaps 3;

QY 21 TALPLDGDQPADRPAPERMDDISSDEHPLFDKRNCCNGCCSSKWCPRDHPAR-CCG 74
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RESULT 14
US-10-029-217A-24
; Sequence 24, Application US/10029217A
; Patent No. US20020164735A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC N.
; APPLICANT: WANG, DA-ZHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO A CARDIAC-SPECIFIC
; FILE REFERENCE: NUCLEAR REGULATORY FACTOR
; FILE REFERENCE: UTSD:6950S
; CURRENT APPLICATION NUMBER: US/10/029,217A
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; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/257,761
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 3907
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-029-217A-24

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Best Local Similarity 44.4%; Pred. No. 4.4e+02;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 56 CCNGGCGSSKWCPRDHPARCC 73
Db 535 CCGGCGAGACGACGCTCC 552

RESULT 15
US-09-894-882-212
; Sequence 212, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 212
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Conus lyneceus
US-09-894-882-212

Query Match 13.7%; Score 57.5; DB 10; Length 71;
Best Local Similarity 26.6%; Pred. No. 7.3;
Matches 17; Conservative 10; Mismatches 24; Indels 13; Gaps 2;

QY 11 LTVCLLILPLTALPLDGDQPADRPAPERMDDISSDEHPLFDKRNCCNGCCSSKWCPRDHA 70
Db 3 LCVTFLLVLTLPSTVTGKSSMRTLNR-----LLKRNWSWCSG--SGEGCDYHS 49

QY 71 RCCG 74
Db 50 ECCG 53

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Job time : 118.087 secs
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Best Local Similarity    25.3%;   Pred. No. 54;
Matches      21; Conservative     10; Mismatches       28; Indels        24; Gaps         4;

QY          8 GVLTIVCLLLFPPTALPLDGDQPADRPAAERMODDISSDE-----HPL 49
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Db           7 GA VITLC L WLAASGGLAAG--PGAAAARRLDESLSAGSVQRAPCASRCLSLOITRISAF 64

QY          50 FDKRNCCNGCGCSKWC RDHARC 72
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Db           65 FOHFQN--NG--SLVWCONHKQC 83


RESULT 7
US-09-826-508-3
; Sequence 3, Application US/09826508
; Patent No. US20010025099A1
; GENERAL INFORMATION:
; APPLICANT: Nabil Elshourbagy
; APPLICANT: Lisa Vawter
; TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides
; TITLE OF INVENTION: and polynucleotides
; FILE REFERENCE: GP-70744USB
; CURRENT APPLICATION NUMBER: US/09/826,508
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1200
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-826-508-3
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RESULT 8
US-09-925-300-1361
; Sequence 1361, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1361
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1361

Query Match      13.9%; Score 58.5; DB 10; Length 137;
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QY      64      KWCRDHARCC 73

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RESULT 5
US-09-738-626-5612
; Sequence 5612, Application US/09738626

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2003, 08:33:07 ; Search time 116.087 Seconds
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Perfect score: 420

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Searched: 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	60.5	14.4	189	9 US-09-965-528-14	Sequence 14, Appl
4	60.5	14.4	189	9 US-10-028-072-232	Sequence 232, App
5	59.5	14.2	319	9 US-09-738-626-5612	Sequence 5612, Ap
6	59	14.0	679	12 US-10-119-714-1	Sequence 1, Appli
7	59	14.0	1200	10 US-09-826-508-3	Sequence 3, Appli
8	58.5	13.9	137	10 US-09-925-300-1361	Sequence 1361, Ap
9	58.5	13.9	621	10 US-09-925-301-1416	Sequence 1416, Ap
10	58.5	13.9	4679	10 US-09-804-898-2	Sequence 2, Appli
11	58	13.8	80	9 US-09-749-637A-86	Sequence 86, Appl
12	58	13.8	271	10 US-09-745-763-77	Sequence 77, Appl
13	58	13.8	312	10 US-09-925-301-1351	Sequence 1351, Ap
14	58	13.8	3907	9 US-10-029-217A-24	Sequence 24, Appl
15	57.5	13.7	71	10 US-09-894-882-212	Sequence 212, App
16	57.5	13.7	297	10 US-09-925-302-609	Sequence 609, App
17	57.5	13.7	1164	10 US-09-046A-2	Sequence 2, Appli
18	57	13.6	108	9 US-09-950-933A-61	Sequence 61, Appl
19	57	13.6	117	9 US-09-950-933A-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1

US-10-096-961-1
; Sequence 1, Application US/10096961
; Patent No. US20020155572A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al.
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE OF INVENTION: CL000849DIV
; FILE REFERENCE: CL000849DIV
; CURRENT APPLICATION NUMBER: US/10/096,961
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/232,632
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 09/738,884
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2211
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-096-961-1

Query Match 14.8%; Score 62; DB 9; Length 2211;
Best Local Similarity 52.6%; Pred. No. 89;
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 56 CCNGGSSKWCROHARCCG 74

Db 47 CCCGGCTCCGCAAGATCCG 65

RESULT 2

US-09-920-897-4
; Sequence 4, Application US/09920897
; Patent No. US20020009489A1
; GENERAL INFORMATION:
; APPLICANT: Paslin, David A.
; TITLE OF INVENTION: ATOPIC DERMATITIS METHOD
; FILE REFERENCE: 17761-702
; CURRENT APPLICATION NUMBER: US/09/920,897

Sequence 8, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 470, App
Sequence 498, App
Sequence 274, App
Sequence 11, Appl
Sequence 15, Appl
Sequence 63, Appl
Sequence 2, Appli
Sequence 265, App
Sequence 39, Appl
Sequence 484, App
Sequence 4912, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 56, Appl
Sequence 65, Appl
Sequence 246, App
Sequence 246, App
Sequence 44, Appl
Sequence 246, App